

From: Swope, Sheridan  
Sent: Friday, October 22, 2004 3:41 PM  
To: STIC-Biotech/ChemLib  
Cc: Schreiber, David  
Subject: 09/980,881

Please forward to David Schreiber

David,

For 09/980,881,

pls search and interference search:

SID 9 against the NT and AA data bases, wherein the maximum length of the polypeptide hit is 19 amino acids and the maximum length of the polynucleotide hit is 57 nucleotides.

pls interference search only:

SID 1, residues 18-1097, against the NT and AA data bases  
SID 2 full-length regular and oligo against the NT and AA data bases  
SID 3 full-length regular and oligo against the NT and AA data bases  
SID 4 full-length regular and oligo against the NT and AA data bases

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
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Searcher Phone: 2-\_\_\_\_\_  
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Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 00:07:08 ; Search time 380 Seconds  
(without alignments)  
193.400 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVKKLLPLSLK 14

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 4074946

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2/1/USPIO.spool/US09980881/runat\_28102004\_131502\_11391/app\_query.fasta\_1.199  
-DB=N Geneseq\_23Sep04 -Qfmt=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=plo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=57  
-USFR=US09980881 @CGN 1 1 470 @runat\_28102004\_131502\_11391 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_23Sep04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	65.7	43	4 AAF80298	Aaf80298 PCR prime
C 2	37	52.9	41	6 ABZ48454	Abz48454 Human org
C 3	37	52.9	51	2 AAT00624	Aat00624 Human (2
C 4	36	51.4	36	10 ADD69569	Add69569 Food enri
C 5	36	51.4	36	10 ADD69568	Add69568 Food enri
C 6	36	51.4	51	4 AAL27400	Aal27400 Human SNP

7	35.5	50.7	39	2	AAQ36595	Aaq36595 PCR prime
C 8	35	50.0	45	2	AAZ33905	Aaz33905 Human PRO
C 9	35	50.0	45	3	AAC78611	Aac78611 Human PRO
C 10	35	50.0	45	6	ABK40321	Abk40321 Oligonuc1
C 11	35	50.0	45	8	ACA63473	Aca63473 Novel hum
C 12	35	50.0	45	8	ACA71637	Aca71637 Human PRO
C 13	35	50.0	45	8	ABX92277	Abx92277 Human PRO
C 14	35	50.0	45	8	ACA66018	Aca66018 Human sec
C 15	35	50.0	45	9	ADA24556	Ada24556 Secreted
C 16	35	50.0	45	9	ACD29619	Acd29619 Novel hum
C 17	35	50.0	45	9	ADA12217	Ada12217 Human sec
C 18	35	50.0	45	9	ACD29034	Acd29034 Novel hum
C 19	35	50.0	45	10	ADB73523	Adb73523 Human PRO
C 20	35	50.0	45	10	ADB76239	Adb76239 Human PRO
C 21	35	50.0	45	10	ADC43665	Adc43665 Human PRO
C 22	35	50.0	45	10	ADC61425	Adc61425 Human PRO
C 23	35	50.0	45	10	ADC63389	Adc63389 Human PRO
C 24	35	50.0	45	10	ADC66489	Adc66489 Human PRO
C 25	35	50.0	45	10	ADC68613	Adc68613 Human PRO
C 26	35	50.0	45	10	ADC62673	Adc62673 Human PRO
C 27	35	50.0	45	10	ADC67738	Adc67738 Human PRO
C 28	35	50.0	45	10	ADC41058	Adc41058 Human PRO
C 29	35	50.0	45	10	ADC67113	Adc67113 Human PRO
C 30	35	50.0	45	10	ADC62049	Adc62049 Human PRO
C 31	35	50.0	45	10	ADC41682	Adc41682 Human PRO
C 32	35	50.0	45	10	ADE49051	Adc49051 Human PRO
C 33	35	50.0	45	10	ADE35105	Adc35105 Human PRO
C 34	35	50.0	45	10	ADE16219	Adc16219 Human PRO
C 35	35	50.0	45	10	ADD72834	Adc72834 Human PRO
C 36	35	50.0	45	10	ADD72192	Adc72192 Human PRO
C 37	35	50.0	45	10	ADE16843	Adc16843 Human PRO
C 38	35	50.0	45	10	ADF46857	Adf46857 Human PRO
C 39	35	50.0	45	10	ADG52614	Adg52614 Human PRO
C 40	35	50.0	45	10	ADG59934	Adg59934 Human PRO
C 41	35	50.0	45	10	ADI60894	Adi60894 Human PRO
C 42	35	50.0	45	10	ADJ37384	Adj37384 Tumour th
C 43	35	50.0	45	10	ACD42438	Acd42438 Novel hum
C 44	35	50.0	45	12	ADE48351	Ade48351 Human PRO
C 45	35	50.0	45	12	ADB89452	Ade89452 Human PRO

#### ALIGNMENTS

##### RESULT 1

AAF80298/c  
ID AAF80298 standard; DNA; 43 BP.

XX AAF80298;

XX AAF80298;

29-JUN-2001 (first entry)

DE PCR primer used to amplify the RK2 origin of replication.

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;

KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant;

KW PCR primer; ss.

XX Escherichia coli.

XX FR2798139-Al.

PN 09-MAR-2001.

XX 03-SEP-1999; 99FR-00011112.

XX 03-SEP-1999; 99FR-00011112.

XX (MERI-) MERISTEM THERAPEUTICS SA.

XX Gruber V, Comeau D;

XX WPI; 2001-259847/27.

PT New vector free from non-essential elements, useful for transforming  
 PT cells for protein production and for preparing transgenic plants.  
 XX  
 PS Example 1; Page 13; 180pp; French.  
 XX  
 CC The specification describes a synthetic vector containing only those  
 CC elements essential for its functionality and transgenesis of a cell  
 CC (especially a plant cell). The vector consists of at most one origin of  
 CC replication (ori), at most one sequence encoding a selection agent and a  
 CC trfA locus encoding a protein that increases the level of plasmid  
 CC replication. The vector particularly contains an RK2 ori, especially oriV  
 CC from PRK2 of *Escherichia coli* with a broad host range, an antibiotic  
 CC resistance gene (especially nptII) conferring resistance to kanamycin in  
 CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.  
 CC The vectors are used to prepare transgenic plants and transformed host  
 CC cells for production of a heterologous proteins, e.g. insulin,  
 CC interferon, lipase, blood proteins and anti-inflammatory agents. PCR  
 CC primers AAF80297-98 were used to amplify the RK2 ori, and the amplified  
 CC fragment was used to construct plasmids of the invention  
 XX  
 SQ Sequence 43 BP; 11 A; 6 C; 17 G; 9 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.67 Length: 43  
 Score: 46.00 Matches: 9  
 Percent Similarity: 90.91% Conservative: 1  
 Best Local Similarity: 81.82% Mismatches: 1  
 Query Match: 65.71% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-980-881A-9 (1-14) x AAF80298 (1-43)  
 Qy 1 SerAsnProValGluLysLeuLeuProLeu 11  
 Db 38 TCGAACCTCCCGTGAAGGCTTCTACCATTA 6  
 RESULT 2  
 ABZ48454/C  
 ID ABZ48454 standard; DNA; 41 BP.  
 AC ABZ48454;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human organic cation transporter OCT1 gene polymorphic site, #5237.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
 KW drug evaluation; drug screening; genotyping; genetic profiling;  
 KW therapeutic customisation; adverse reaction; clinical trial;  
 KW drug approval; single nucleotide polymorphism; SNP; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT variation replace(21,T)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200252044-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 27-DEC-2001; 2001WO-JP011592.  
 XX  
 PR 27-DEC-2000; 2000JP-00399443.  
 PR 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 KW (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 XX  
 WPI; 2002-583571/62.  
 XX

XX  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX  
 PS Claim 23; Page 166; 2785pp; English.  
 XX  
 CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy.  
 XX  
 SQ Sequence 41 BP; 11 A; 11 C; 13 G; 6 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 276 Length: 41  
 Score: 37.00 Matches: 7  
 Percent Similarity: 77.78% Conservative: 0  
 Best Local Similarity: 77.78% Mismatches: 2  
 Query Match: 52.86% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-980-881A-9 (1-14) x ABZ48454 (1-41)  
 Qy 3 ProProValGluLysLeuLeuProLeu 11  
 Db 33 CCACCTGTGGAGCCTTCTTCCATCCTG 7  
 RESULT 3  
 AAT00624  
 ID AAT00624 standard; DNA; 51 BP.  
 XX  
 AC AAT00624;  
 XX  
 DT 03-FEB-1996 (first entry)  
 XX  
 DE Human (2'-5') oligo A synthetase antigenic peptide cDNA.  
 XX  
 KW (2'-5') oligo A synthetase; interferon; antigenic peptide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CAl337281-C.



XX 10-OCT-1995.  
 XX  
 XX 18-APR-1985; 85CA-00479458.  
 XX  
 XX 18-APR-1984; 84US-00601782.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Revel M, Chebath J;  
 XX  
 XX WPI; 1995-366737/48.  
 DR P-PSDB; AAR84190.  
 XX  
 XX New DNA encoding 2'-5' oligo A synthetase and related vectors -  
 PT transformed microorganisms, proteins and antigenic peptide(s), useful for  
 PT monitoring interferon activity in cells and body fluids.  
 XX  
 XX Claim 7; Fig 7a; 75pp; English.  
 XX  
 XX Enzyme AAR84186 has a mol.wt. of about 41,500 daltons, AA sequence  
 CC AAR84186 is claimed. Also claimed is the antigenic peptide AAR84190 which  
 CC is AAs 348-364 of AAR84186. A DNA molecule coding for a C-terminal  
 CC heptadecapeptide of (2'-5') oligo A synthetase comprising nts 1075-1124  
 CC of AAT00619 is claimed. This encodes AAR84190, and its sequence is given  
 CC in AAT00624. For further information see AAR84186 and AAT00619  
 XX  
 XX SQ Sequence 51 BP; 7 A; 24 C; 6 G; 14 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 355 Length: 51  
 Score: 37.00 Matches: 7  
 Percent Similarity: 66.67% Conservative: 1  
 Best Local Similarity: 58.33% Mismatches: 4  
 Query Match: 52.86% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-980-881A-9 (1-14) x AAT00624 (1-51)  
 Qy 3 ProValGluLysLeuLeuProLeuSerLeuLys 14  
 Db 14 CCTCCCTGCCATTCATCCCTGCCCCCTCTCCATGAAG 49  
 RESULT 4  
 ADD69569  
 ID ADD69569 standard; DNA; 36 BP.  
 XX  
 XX ADD69569;  
 XX  
 XX 15-JAN-2004 (first entry)  
 XX  
 XX Food enrichment-related PCR primer QCR1 - SEQ ID 49.  
 XX  
 XX food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;  
 XX PCR; primer; ss; QCR1.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2003080832-A1.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 26-MAR-2003; 2003WO-JP003715.  
 XX  
 XX 26-MAR-2002; 2002JP-00085058.  
 XX  
 XX (AJIN ) AJINOMOTO CO INC.  
 XX  
 XX Nishiuchi H, Nishimura Y, Kuroda M;  
 XX  
 XX WPI; 2003-833508/77.  
 XX  
 XX 26-MAR-2003; 2003WO-JP003715.  
 XX  
 XX 26-MAR-2002; 2002JP-00085058.  
 XX  
 XX (AJIN ) AJINOMOTO CO INC.  
 XX  
 XX Nishiuchi H, Nishimura Y, Kuroda M;  
 XX  
 XX WPI; 2003-833508/77.  
 XX  
 XX Genetically-modified Candida utilis for producing foods and drinks

PT enriched with gamma-glutamyl cysteine or cysteine, useful in food  
 PT industry e.g. for seasoning, by culturing and processing to enhance  
 XX flavor.  
 XX  
 XX Example 3; SEQ ID NO 49; 70pp; Japanese.  
 XX  
 XX The invention relates to a novel method for producing a food containing  
 CC gamma-glutamyl cysteine or cysteine comprising culturing under  
 CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or  
 CC more by weight of gamma-glutamyl cysteine based on dry cells in the  
 CC logarithmic growth phase when cultured in the minimum medium, adding the  
 CC obtained culture, optionally after heating, to a food or drink material  
 CC and processing. The yeast of the invention may be used for producing food  
 CC and drink with enriched gamma-glutamyl cysteine or cysteine which is  
 CC useful in food industry e.g. for seasoning. In this way, food and drink  
 CC can be cheaply produced with improved flavour. The current sequence is  
 CC that of the food enrichment-related PCR primer of the invention.  
 XX  
 XX SQ Sequence 36 BP; 16 A; 9 C; 4 G; 7 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 352 Length: 36  
 Score: 36.00 Matches: 7  
 Percent Similarity: 72.73% Conservative: 1  
 Best Local Similarity: 63.64% Mismatches: 3  
 Query Match: 51.43% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-980-881A-9 (1-14) x ADD69569 (1-36)  
 Qy 4 ProValGluLysLeuLeuProLeuSerLeuLys 14  
 Db 4 CCTATTGAAATAATTACTACCCCAAGAAAG 36  
 RESULT 5  
 ADD69568/c  
 ID ADD69568 standard; DNA; 36 BP.  
 XX  
 XX ADD69568;  
 XX  
 XX 15-JAN-2004 (first entry)  
 XX  
 XX Food enrichment-related PCR primer QCF1 - SEQ ID 48.  
 XX  
 XX food; gamma-glutamyl cysteine; drink; seasoning; flavour improvement;  
 XX PCR; primer; ss; QCF1.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2003080832-A1.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 26-MAR-2003; 2003WO-JP003715.  
 XX  
 XX 26-MAR-2002; 2002JP-00085058.  
 XX  
 XX (AJIN ) AJINOMOTO CO INC.  
 XX  
 XX Nishiuchi H, Nishimura Y, Kuroda M;  
 XX  
 XX WPI; 2003-833508/77.  
 XX  
 XX Genetically-modified Candida utilis for producing foods and drinks  
 PT enriched with gamma-glutamyl cysteine or cysteine, useful in food  
 PT industry e.g. for seasoning, by culturing and processing to enhance  
 XX flavor.  
 XX  
 XX Example 3; SEQ ID NO 48; 70pp; Japanese.  
 XX  
 XX The invention relates to a novel method for producing a food containing  
 CC gamma-glutamyl cysteine or cysteine comprising culturing under  
 CC appropriate conditions Candida utilis (Pichia jadinii) containing 1% or



Alignment Scores:  
Pred. No.: 469 Length: 39  
Score: 35.50 Matches: 9  
Percent Similarity: 83.33% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 50.71% Indels: 1  
DB: 2 Gaps: 1

US-09-980-881A-9 (1-14) x AAQ36595 (1-39)

Qy 3 ProProValGluLysLeuLeuProLeuSerLeuLys 14  
Db 5 CCCCCTGGTG---AAGCTGCTACCTCTTGACAGAAA 37

RESULT 8

ID AAZ33905/C  
XX AAZ33905 standard; DNA; 45 BP.

AC AAZ333905;

DT 07-DEC-1999 (first entry)

XX Human PRO274 hybridisation probe.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077641P.

XX 12-MAR-1998; 98US-0077791P.

XX 13-MAR-1998; 98US-0078004P.

XX 17-MAR-1998; 98US-00040220.

XX 20-MAR-1998; 98US-0078886P.

XX 20-MAR-1998; 98US-0078910P.

XX 20-MAR-1998; 98US-0078936P.

XX 20-MAR-1998; 98US-0078939P.

XX 25-MAR-1998; 98US-0079294P.

XX 26-MAR-1998; 98US-0079656P.

XX 27-MAR-1998; 98US-0079663P.

XX 27-MAR-1998; 98US-0079664P.

XX 27-MAR-1998; 98US-0079689P.

XX 27-MAR-1998; 98US-0079728P.

XX 27-MAR-1998; 98US-0079786P.

XX 30-MAR-1998; 98US-0079920P.

XX 30-MAR-1998; 98US-0079923P.

XX 31-MAR-1998; 98US-0080105P.

XX 31-MAR-1998; 98US-0080107P.

XX 31-MAR-1998; 98US-0080165P.

XX 31-MAR-1998; 98US-0080194P.

XX 01-APR-1998; 98US-0080327P.

XX 01-APR-1998; 98US-0080328P.

XX 01-APR-1998; 98US-0080333P.

XX 01-APR-1998; 98US-0080334P.

XX 08-APR-1998; 98US-0081049P.

XX 08-APR-1998; 98US-0081070P.

XX 08-APR-1998; 98US-0081071P.

XX 09-APR-1998; 98US-0081185P.

XX 09-APR-1998; 98US-0081203P.

XX 09-APR-1998; 98US-0081229P.

XX 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 03-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084411P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085589P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

(GETH ) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

New secreted and transmembrane polypeptides and their polynucleotides,  
useful for treating blood coagulation disorders, cancers and cellular  
adhesion disorders.

Example 4; Page 184; 530pp; English.

The present invention describes secreted and transmembrane polypeptides  
and their polynucleotides. The nucleotide sequences are useful as sources  
of probes, primers, for chromosome mapping, and for generation of  
antisense sequences. They can also be used to create transgenic animals.  
The proteins can be used to treat a variety of diseases and disorders,  
depending on their function. Diseases that may be treated include blood  
coagulation disorders, cancers and cellular adhesion disorders. They may

CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AA41685 to  
 CC AA41774 represent polynucleotide and polypeptide sequence given in the  
 CC exemplification of the present invention

XX SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 672 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x AAZ33905 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 9

AAAC78611/c

ID AAC78611 standard; DNA; 45 BP.

XX AC AAC78611;

XX DT 08-FEB-2001 (first entry)

XX DE Human PRO274 hybridisation probe SEQ ID NO:17.

XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 XX expressed sequence tag; detection; cancer; PCR primer; probe; ss.

XX OS Homo sapiens.

XX PN WO200053756-A2.

XX PD 14-SEP-2000.

XX PF 18-FEB-2000; 2000WO-US004341.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 12-MAR-1999; 99US-0123957P.

XX PR 29-MAR-1999; 99US-0126773P.

XX PR 21-APR-1999; 99US-0130232P.

XX PR 28-APR-1999; 99US-0131445P.

XX PR 14-MAY-1999; 99US-0134287P.

XX PR 23-JUN-1999; 99US-0141037P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 29-OCT-1999; 99US-0162506P.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 16-DEC-1999; 99WO-US028565.

XX PR 30-DEC-1999; 99WO-US030095.

XX PR 30-DEC-1999; 99WO-US031243.

XX PR 05-JAN-2000; 99WO-US031274.

XX PR 06-JAN-2000; 2000WO-US000219.

XX PR 06-JAN-2000; 2000WO-US000277.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX PI Ferraz N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

XX PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;

XX PI Stewart TA, Tumas D, Williams PM, Wood WI;

XX DR WPI; 2000-611443/58.

XX PT Novel PRO polypeptides and polynucleotides used in detection methods, to

XX target bioactive molecules to specific cells, and to modulate cellular

XX PT activities.

XX PS Example 4; Page 235; 636pp; English.

XX CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences

XX SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 672 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x AAC78611 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 10

ABK40321/c

ID ABK40321 standard; DNA; 45 BP.

XX AC ABK40321;

XX DT 15-JUL-2002 (first entry)

XX DE Oligonucleotide probe for human PRO274 DNA.

XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
 KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
 KW neuroprotective; probe; ss.

XX OS Homo sapiens.

XX PN WO200153486-A1.

XX PD 26-JUL-2001.

XX PF 11-FEB-2000; 2000WO-US003565.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 11-MAR-1999; 99US-0123972P.

XX PR 11-MAY-1999; 99US-0133459P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 22-JUN-1999; 99US-0140650P.

XX PR 20-JUL-1999; 99US-0140653P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 28-JUL-1999; 99US-0146222P.

XX PR 17-AUG-1999; 99US-0149395P.

XX PR 31-AUG-1999; 99US-0151689P.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PA (GETH ) GENENTECH INC.

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XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX Example 10; Page 120; 302pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC antibodies are useful for treating benign or malignant tumours (e.g.
CC renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC malignancies, other disorders such as neuronal, glial, astrocytal,
CC hypothalamic, glandular, macrophagal, stromal and blastococic disorders,
CC inflammatory, immune and angiogenic disorders. The polynucleotide
CC sequences are also useful in gene therapy. The present sequence
CC represents a probe used in the methods of the present invention
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      672      Length:      45
Score:          35.00    Matches:      7
Percent Similarity: 80.00%  Conservative: 1
Best Local Similarity: 70.00%  Mismatches:  2
Query Match:      50.00%    Indels:      0
DB:              6        Gaps:      0

US-09-980-881a-9 (1-14) x ABK40321 (1-45)

Qy 1 SetAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 11
ACA63473/c
ID ACA63473 standard; DNA; 45 BP.
XX
AC ACA63473;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein related probe #2.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; probe; ss.
XX
OS Homo sapiens.
XX
FN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 08-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US028565.
PR 30-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.

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PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Aehkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillian KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-328860/31.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Example 4; Page 125; 453pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence represents a novel human secreted and
XX transmembrane PRO polypeptide associated probe
XX
XX Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;
SQ
```

Alignment Scores:			
Pred. No.:	672	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	8	Gaps:	0

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US-09-980-881A-9 (1-14) x ACA63473 (1-45)
Qy 1 SerAsnProProValGluLysLeuLeuPro 10
   ||||| ||||| ||||| ||||| |||||
Db 32 AGCAATGCCCGTTCAGGCGTCTCTCCCC 3
RESULT 12
ACA71637/C
ID ACA71637 standard; DNA; 45 BP.
XX
XX ACA71637;
XX
XX 11-AUG-2003 (first entry)
DT
XX
XX Human PRO polypeptide associated oligonucleotide SEQ ID NO 17.
XX
XX Human; ds; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW
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KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
XX Homo sapiens.
XX
XX US2002177553-A1.
XX
XX 28-NOV-2002.
XX
XX 15-OCT-2001; 2001US-00978192.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 26-JUN-1998; 98US-00105413.
XX 07-OCT-1998; 98US-00169978.
XX 07-OCT-1998; 98WO-US021141.
XX 06-NOV-1998; 98US-00184216.
XX 06-NOV-1998; 98US-00187368.
XX 07-DEC-1998; 98WO-US024855.
XX 07-DEC-1998; 98US-00202054.
XX 22-DEC-1998; 98US-00218517.
XX 05-JAN-1999; 99WO-US000106.
XX 05-MAR-1999; 99US-00254465.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-00265686.
XX 10-MAR-1999; 99WO-US005190.
XX 12-MAR-1999; 99US-00267213.
XX 12-APR-1999; 99US-00284291.
XX 14-MAY-1999; 99US-00311832.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 25-AUG-1999; 99US-00380137.
XX 25-AUG-1999; 99US-00380138.
XX 25-AUG-1999; 99US-00380142.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000WO-US006519.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.
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PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000US-00709238.  
PR 27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 22-MAR-2001; 2001WO-US009552.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
XX Stewart TA, Tunas D, Williams PW, Wood WI;  
XX  
XX WPI; 2003-328499/31.  
XX  
XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as  
XX pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying  
XX modulators of receptor-ligand interactions.  
XX  
XX Disclosure; SEQ ID NO 17; 55pp; English.  
XX  
XX The invention relates to an isolated secreted and transmembrane  
XX polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful  
XX in PRO polypeptide detection methods. The PRO polypeptide is useful for  
XX linking a bioactive molecule to a cell. The PRO polypeptide or an  
XX antibody against it is useful for modulating a biological activity of a  
XX cell. The PRO polypeptide is useful in industrial applications including  
XX pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO  
XX polypeptide is also useful as a thrombolytic agent, interferon,  
XX interleukin, erythropoietin, colony stimulating factor and other  
XX cytokines. The PRO polypeptide is useful for treating disease such as  
XX cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,  
XX amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,  
XX atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,  
XX Parkinson's disease; cardiovascular disease e.g. hypertension and  
XX myocardial ischemia; kidney disease e.g. renal failure and  
XX glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial  
XX asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory  
XX bowel disease; reproductive disorders e.g. premature labour and  
XX preclampsia; carcinogenesis. The present sequence represents a PRO  
XX polypeptide associated oligonucleotide of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format directly from USPTO  
XX at seqdata.uspto.gov/sequence.html?docid=20020177553  
XX  
XX Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 672 Length: 45  
XX Score: 35.00 Matches: 7  
XX Percent Similarity: 80.00% Conservative: 1

Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 8 Gaps: 0  
US-09-980-881A-9 (1-14) x ACA71637 (1-45)  
Qy 1 SerAsnProProValGluLysLeuLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3  
RESULT 13  
ABX92277/c  
ID ABX92277 standard; DNA; 45 BP.  
XX AC ABX92277;  
XX  
XX 08-MAY-2003 (first entry)  
XX Human PRO DNA probe SEQ ID No 17.  
XX Human; PRO polypeptide; secreted and transmembrane protein;  
XX immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
XX cardiac insufficiency; nervous system disorder; kidney disorder;  
XX bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
XX genetic disorder; cytostatic; anti-diabetic; anti-inflammatory;  
XX anti-arthritis; anti-tumour; vulnery; antianaemic; dermatological;  
XX cardiant; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002169284-A1.  
XX  
XX 14-NOV-2002.  
XX  
XX 16-OCT-2001; 2001US-00978697.  
XX  
XX 26-MAY-1981; 81US-00267213.  
XX 17-OCT-1997; 97US-0062250P.  
XX 03-NOV-1997; 97US-0064249P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 21-NOV-1997; 97US-0066364P.  
XX 10-MAR-1998; 98US-0077450P.  
XX 11-MAR-1998; 98US-0077632P.  
XX 11-MAR-1998; 98US-0077641P.  
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XX 13-MAR-1998; 98US-0078004P.  
XX 17-MAR-1998; 98US-00040220.  
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XX 30-MAR-1998; 98US-0079920P.  
XX 30-MAR-1998; 98US-0079923P.  
XX 26-JUN-1998; 98US-00105413.  
XX 07-OCT-1998; 98US-00168978.  
XX 07-OCT-1998; 98WO-US021141.  
XX 06-NOV-1998; 98US-00184216.  
XX 06-NOV-1998; 98US-00187368.  
XX 20-NOV-1998; 98WO-US024855.  
XX 07-DEC-1998; 98US-00202054.  
XX 22-DEC-1998; 98US-00218517.  
XX 03-JAN-1999; 99WO-US000106.  
XX 05-MAR-1999; 99US-00254465.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99US-00265686.







XX 20-NOV-2003 (first entry)  
DT Secreted and transmembrane PRO protein associated probe #2.  
XX  
DE Human; secreted and transmembrane protein; PRO; tissue typing;  
XX chromosome identification; vaccine; cancer; retinal disorder;  
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;  
KW wound healing; obesity; diabetes; hearing loss;  
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;  
KW haemoglobin associated disorder; probe; ss.  
XX  
OS Homo sapiens.  
XX  
FN US2003050241-A1.  
XX  
XX 13-MAR-2003.  
XX  
PF 16-OCT-2001; 2001US-00978564.  
XX  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
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PR 28-MAY-1998; 98US-0087098P.  
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PR 08-MAR-1999; 99WO-US005028.  
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PR 26-APR-1999; 99US-0131022P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.  
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PR 02-JUN-1999; 99WO-US012252.  
PR 16-JUN-1999; 99US-0139557P.  
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PR 07-JUL-1999; 99US-0142680P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.

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PR 11-FEB-2000; 200WO-US003565.
PR 18-FEB-2000; 200WO-US004341.
PR 24-FEB-2000; 200WO-US005004.
PR 02-MAR-2000; 200WO-US005841.
PR 10-MAR-2000; 200WO-US006319.
PR 21-MAR-2000; 200WO-US007532.
PR 30-MAR-2000; 200WO-US008439.
PR 17-MAY-2000; 200WO-US013705.
PR 22-MAY-2000; 200WO-US014042.
PR 30-MAY-2000; 200WO-US014941.
PR 02-JUN-2000; 200WO-US015264.
PR 28-JUL-2000; 200WO-US020710.
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PR 01-DEC-2000; 200WO-US032678.
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PR 28-FEB-2001; 200WO-US006520.
PR 22-MAR-2001; 200WO-US009552.
PR 25-MAY-2001; 200WO-US017092.
PR 01-JUN-2001; 200WO-US017800.
PR 20-JUN-2001; 200WO-US019692.
PR 29-JUN-2001; 200WO-US021066.
PR 09-JUL-2001; 200WO-US021735.
PR 30-JUL-2001; 200WO-US021858.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
XX
XX New isolated PRO polypeptides for example extracellular, secreted and
XX membrane bound proteins, useful for modulating the biological activities
XX of cells and for treating, for example diabetes, cancer, rheumatoid
XX arthritis, and hearing loss.
XX
XX Example 4; Page 132; 461pp; English.
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
XX polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
XX polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
XX useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
XX useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
XX useful for linking a bioactive molecule to a cell expressing a PRO337
XX polypeptide, and PRO337 is useful for linking a bioactive molecule to a
XX cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
XX bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
XX polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for
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XX Score: 35.00 Matches: 7
XX Percent Similarity: 80.00% Conservative: 1
XX Best Local Similarity: 70.00% Mismatches: 2
XX Query Match: 50.00% Indels: 0
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XX Job time : 386 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:21:49 ; Search time 38 Seconds  
(without alignments)  
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Searched: 478139 seqs, 66318000 residues

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#### SUMMARIES

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4	30	42.9	14	3	US-09-248-061B-27
5	29	41.4	18	2	US-08-480-190-204
6	29	41.4	18	2	US-08-488-379-204
7	29	41.4	18	4	US-08-475-399A-204
8	29	41.4	18	4	US-08-077-255A-204
9	29	41.4	18	5	PCT-US93-07545-204
10	28	40.0	5	1	US-08-477-509B-13
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22	27	38.6	16	4	US-09-715-923-8
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24	26.5	37.9	16	4	US-09-500-124-204
25	26	37.1	9	1	US-08-615-181-100
26	26	37.1	10	4	US-08-983-157B-8
27	26	37.1	10	4	US-09-653-465B-11

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Sequence 43, Appl  
Sequence 121, App  
Sequence 79, Appl  
Sequence 1, Appl  
Sequence 15, Appl  
Sequence 100, App  
Sequence 322, App  
Sequence 156, App  
Sequence 322, App  
Sequence 156, App  
Sequence 33, Appl  
Sequence 71, Appl  
Sequence 34, Appl

#### ALIGNMENTS

RESULT 1  
US-08-964-725-15  
; Sequence 15, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STRUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: No. 5939265e
US-08-964-725-15

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Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLSL 13
Db 6 PVDKLAFLPL 15

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US-09-007-288E-88
; Sequence 88, Application US/09007288E
; Patent No. 6495357
; GENERAL INFORMATION:
; APPLICANT: Fugleang, Claus
; APPLICANT: Okkels, Jens
; APPLICANT: Petersen, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Thellersen, Marianne
; APPLICANT: Svenden, Allan
; APPLICANT: Borch, Kim
; APPLICANT: Royer, John
; APPLICANT: Kretschmar, Titus
; APPLICANT: Halkier, Torben
; APPLICANT: Vind, Jesper
; APPLICANT: Jorgensen, Steen
; TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes
; FILE REFERENCE: 4455.404-US
; CURRENT APPLICATION NUMBER: US/09/007.288E
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide addition
US-09-007-288E-88

Query Match      47.1%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 3 PPRRLPLS 12

RESULT 3
US-09-400-653A-31
; Sequence 31, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kaetan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/1F142
; CURRENT APPLICATION NUMBER: US/09/400.653A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248.061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-400-653A-31

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 4
US-09-248-061B-27
; Sequence 27, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S-T.
; APPLICANT: Lim, D-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/248.061B
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-27

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 5
US-08-480-190-204
; Sequence 204, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 515SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-204

Query Match 41.4%; Score 29; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLS 12
Db 3 PYKEVPLS 11

RESULT 6
US-08-488-379-204
; Sequence 204, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-204

Query Match 41.4%; Score 29; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLS 12
Db 3 PYKEVPLS 11

RESULT 7
US-08-475-399A-204
; Sequence 204, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-204

Query Match 41.4%; Score 29; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLS 12
Db 3 PYKEVPLS 11

RESULT 8
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US-08-077-255A-204
; Sequence 204, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-204

Query Match 41.4%; Score 29; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLPLS 12
Db 3 PYKEVPLS 11

RESULT 9
US-08-077-255A-204
; Sequence 204, Application PC/TUS9307545
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

Query Match 41.4%; Score 29; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLPLS 12
Db 3 PYKEVPLS 11

RESULT 9
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; Sequence 204, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-204

Query Match 41.4%; Score 29; DB 5; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLPLS 12
Db 3 PYKEVPLS 11

RESULT 10
US-08-477-509B-13
; Sequence 13, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
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PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-509B-13

Query Match 40.0%; Score 28; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 11  
US-08-482-085B-13  
; Sequence 13, Application US/08482085B  
; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,085B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-085B-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 12  
US-09-444-791A-13  
; Sequence 13, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/444,791A  
; FILING DATE: 22-No. 6355776-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/482,085  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-444-791A-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
Db 1 PPVEK 5

## RESULT 13

US-08-230-047-31  
Sequence 31, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:  
APPLICANT: Searios III, George H.  
APPLICANT: Ivaashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-31

Query Match 40.0%; Score 28; DB 1; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLPL 11  
Db 6 PPVEQLFLM 14

## RESULT 14

US-09-141-882A-10  
Sequence 10, Application US/09141882A  
Patent No. 6022540  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/141,882A  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/057,928  
FILING DATE: September 4, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: SEMONOW, R.  
REGISTRATION NUMBER: 39,022  
REFERENCE/DOCKET NUMBER: 640100-245  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: peptide  
US-09-141-882A-10

Query Match 40.0%; Score 28; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPPVEKLL 9  
Db 6 NPPPEEFL 13

## RESULT 15

US-09-452-142-10  
Sequence 10, Application US/09452142  
Patent No. 6379553  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2

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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452,142
; FILING DATE: 01-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/141,882
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SEMONOW, R.
; REGISTRATION NUMBER: 39,022
; REFERENCE/DOCKET NUMBER: 640100-249
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: <Unknown>
; TOPOLOGY: LINEAR
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-452-142-10

Query Match      40.0%; Score 28; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NPPVVEKLL 9
Db      6 NPPPEEFL 13
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OM protein - protein search, using sw model

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(without alignments)

36.312 Million cell updates/sec

Title: US-09-980-881A-9

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Maximum Match 100%

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#### SUMMARIES

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3	30	42.9	14	14	US-10-024-123-31
4	29	41.4	15	14	US-10-072-602B-616
5	29	41.4	17	15	US-10-378-089-1
6	28	40.0	5	14	US-10-096-986-13
7	28	40.0	8	15	US-10-182-252A-154
8	28	40.0	9	15	US-10-264-309-397
9	28	40.0	9	15	US-10-182-252A-142
10	28	40.0	9	15	US-10-182-252A-273
11	28	40.0	9	15	US-10-182-252A-796
12	28	40.0	9	15	US-10-182-252A-840
13	28	40.0	9	15	US-10-182-252A-1156

14	28	40.0	9	15	US-10-182-252A-1157	Sequence 1157, Ap
15	28	40.0	9	15	US-10-182-252A-1158	Sequence 1158, Ap
16	28	40.0	9	15	US-10-182-252A-1159	Sequence 1159, Ap
17	28	40.0	9	15	US-10-182-252A-1173	Sequence 1173, Ap
18	28	40.0	9	16	US-10-415-014-516	Sequence 516, App
19	28	40.0	9	16	US-10-415-014-624	Sequence 624, App
20	28	40.0	10	9	US-09-055-744-5	Sequence 5, Appli
21	28	40.0	10	16	US-10-415-014-572	Sequence 572, App
22	28	40.0	12	9	US-09-055-744-7	Sequence 7, Appli
23	28	40.0	14	14	US-10-148-936-2	Sequence 2, Appli
24	28	40.0	16	16	US-10-481-180-682	Sequence 682, App
25	28	40.0	18	9	US-09-880-713A-19	Sequence 19, Appli
26	28	40.0	18	9	US-09-226-248B-9	Sequence 9, Appli
27	27	38.6	8	15	US-10-182-252A-1296	Sequence 1296, Ap
28	27	38.6	9	15	US-10-182-252A-140	Sequence 140, App
29	27	38.6	9	15	US-10-182-252A-272	Sequence 272, App
30	27	38.6	9	15	US-10-182-252A-884	Sequence 884, App
31	27	38.6	9	15	US-10-182-252A-885	Sequence 885, App
32	27	38.6	9	15	US-10-182-252A-899	Sequence 899, App
33	27	38.6	9	15	US-10-182-252A-900	Sequence 900, App
34	27	38.6	10	14	US-10-283-349-51	Sequence 51, Appli
35	27	38.6	12	9	US-09-997-579-10	Sequence 10, Appli
36	27	38.6	12	14	US-10-360-522-6	Sequence 6, Appli
37	27	38.6	14	9	US-09-826-290-224	Sequence 224, App
38	27	38.6	14	14	US-10-162-134A-3	Sequence 3, Appli
39	27	38.6	14	15	US-10-264-309-47	Sequence 47, Appli
40	27	38.6	16	14	US-10-357-479-8	Sequence 8, Appli
41	27	38.6	17	14	US-10-225-567A-753	Sequence 753, App
42	27	38.6	18	14	US-10-225-567A-752	Sequence 752, App
43	27	38.6	19	9	US-09-997-579-8	Sequence 8, Appli
44	26.5	37.9	16	14	US-10-161-791-204	Sequence 204, App
45	26	37.1	8	9	US-09-055-744-4	Sequence 4, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-334-726-111  
; Sequence 111, Application US/10334726  
; Publication No. US20030211521A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE  
; TITLE OF INVENTION: BREAST CANCER ANTIGEN  
; FILE REFERENCE: 1090-36  
; CURRENT APPLICATION NUMBER: US/10/334,726  
; CURRENT FILING DATE: 2003-01-02  
; PRIOR APPLICATION NUMBER: US/09/645,446  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00866  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: GB 9805877.9  
; PRIOR FILING DATE: 1998-09-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:predicted  
; OTHER INFORMATION: peptide  
US-10-334-726-111

Query Match 50.0%; Score 35; DB 14; Length 9;  
Best Local Similarity 75.0%; Pred. NO. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVEKLPL 11

Db 1 PLEKILPL 8

## RESULT 2

US-10-232-544-88  
; Sequence 88, Application US/10232544  
; Publication No. US20030199069A1  
; GENERAL INFORMATION:  
; APPLICANT: Fuglsang, Claus  
; APPLICANT: Okkels, Jens  
; APPLICANT: Petersen, Dorte  
; APPLICANT: Patkar, Shamkant  
; APPLICANT: Thellersen, Marianne  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borch, Kim  
; APPLICANT: Royer, John  
; APPLICANT: Kretzschmar, Titus  
; APPLICANT: Halkier, Torben  
; APPLICANT: Vind, Jesper  
; APPLICANT: Jorgensen, Steen  
; TITLE OF INVENTION: No. US20030199069A1el Lipolytic Enzymes  
; FILE REFERENCE: 4455.404-US  
; CURRENT APPLICATION NUMBER: US/10/232.544  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/007,288  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide addition  
US-10-232-544-88

Query Match 47.1%; Score 33; DB 14; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12  
|||:||||  
Db 3 PPRPRLLPLS 12

## RESULT 3

US-10-024-123-31  
; Sequence 31, Application US/10024123  
; Publication No. US20030022263A1  
; GENERAL INFORMATION:  
; APPLICANT: Kastan, Michael  
; APPLICANT: Canman, Christine  
; APPLICANT: Kim, Seong-Tae  
; APPLICANT: Lim, Dae-Sik  
; APPLICANT: St. Jude Children's Research Hospital  
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
; TITLE OF INVENTION: Therapies  
; FILE REFERENCE: 2427/1P142  
; CURRENT APPLICATION NUMBER: US/10/024.123  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/400,653  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: 09/248,061  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-123-31

Query Match 42.9%; Score 30; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy

3 PPVEKLLPLS 12

|||:||||

Db

4 PPVSQELPCS 13

## RESULT 4

US-10-072-602B-616  
; Sequence 616, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Oliviera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 616  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Conus flavidus  
US-10-072-602B-616

Query Match 41.4%; Score 29; DB 14; Length 15;  
Best Local Similarity 60.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPPVEKLLP 10  
|||||  
Db 4 SNPPCSYLP 13

## RESULT 5

US-10-378-089-1  
; Sequence 1, Application US/10378089  
; Publication No. US20040052780A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KAZUHISA  
; APPLICANT: KAWAMOTO, SEIJI  
; APPLICANT: GOTO, TAKESHI  
; APPLICANT: SATO, SHUJI  
; APPLICANT: GOTO, SIGERU  
; TITLE OF INVENTION: IMMUNOSUPPRESSANT  
; FILE REFERENCE: 7388/80237  
; CURRENT APPLICATION NUMBER: US/10/378,089  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: JP P2002-260661  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-378-089-1

Query Match 41.4%; Score 29; DB 15; Length 17;  
Best Local Similarity 55.6%; Pred. No. 7.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNPPVEXLL 9  
| | | | |  
Db 5 SGPPVSELI 13

RESULT 6  
US-10-096-986-13  
; Sequence 13, Application US/10096986  
; Publication No. US20030083464A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; Richardson, Charles  
; Chambers, James  
; Causey, Stuart  
; Pellock, Thomas J.  
; Cappello, Joseph  
; Crisman, John W.  
; TITLE OF INVENTION: No. US20030083464A1el Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096,986  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/444,791  
; FILING DATE: 22-No. US20030083464A1-1999  
; APPLICATION NUMBER: US 08/482,085  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Treacartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-096-986-13  
Query Match 40.0%; Score 28; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
| | | | |  
Db 1 PPVEK 5

RESULT 7  
US-10-182-252A-154  
; Sequence 154, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-154  
Query Match 40.0%; Score 28; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SNPPV 5  
| | | | |  
Db 2 SNPPV 6  
RESULT 8  
US-10-264-309-397  
; Sequence 397, Application US/10264309  
; Publication No. US20040022794A1  
; GENERAL INFORMATION:  
; APPLICANT: DURHAM, L. KATHRYN  
; APPLICANT: FRIEDMAN, DAVID L.  
; APPLICANT: HERATH, HERATH  
; APPLICANT: KIMMEL, LIDA H.  
; APPLICANT: PAREKH, RAJESH B.  
; APPLICANT: POTTER, DAVID M.  
; APPLICANT: ROHLFF, CHRISTIAN  
; APPLICANT: SILBER, B. MICHAEL  
; APPLICANT: SNYDER, PETER J.  
; APPLICANT: SOARES, HOLLY D.  
; APPLICANT: STIGER, THOMAS R.  
; APPLICANT: SUNDERLAND, P. TREY  
; APPLICANT: TOWNSEND, ROBERT R.  
; APPLICANT: WHITE, W. FROST  
; APPLICANT: WILLIAMS, STEPHEN A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,  
; INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: POA-002.01  
; CURRENT APPLICATION NUMBER: US/10/264,309  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: 60/326,708  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 397

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-397

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LPLSLK 14
Db 4 LPLSLK 9

RESULT 9
US-10-182-252A-142
; Sequence 142, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-142

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 10
US-10-182-252A-273
; Sequence 273, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
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; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-273

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5
Db 3 SNPPV 7

RESULT 11
US-10-182-252A-796
; Sequence 796, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 796
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-796

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEKL 8
Db 4 PPIERL 9

RESULT 12
US-10-182-252A-840
; Sequence 840, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
```



; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 840  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-840

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEKL 8  
||:|:|  
Db 4 PPIERL 9

RESULT 13  
US-10-182-252A-1156  
; Sequence 1156, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1156  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-1156

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
|||||  
Db 3 SNPPV 7

RESULT 14  
US-10-182-252A-1157  
; Sequence 1157, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1157  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-1157

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
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Db 3 SNPPV 7

RESULT 15  
US-10-182-252A-1158  
; Sequence 1158, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1158  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-1158

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPEV 5  
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Db 3 SNPEV 7

Search completed: October 28, 2004, 19:45:44  
Job time : 126 secs



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Percent Similarity: 90.91% Conservative: 1
Best Local Similarity: 81.82% Mismatches: 1
Query Match: 65.71% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX093019 (1-43)

Qy 1 SerAsnProValGluLysLeuLeuProLeu 11
Db 38 TCGAACCCCTCCGTGAAGGCCCTTCTACCATTA 6

RESULT 2
LOCUS AX519039/c 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5237 from Patent WO02052044.
ACCESSION AX519039
VERSION AX519039.1 GI:23569098
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5237 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Alignment Scores:
Pred. No.: 381 Length: 41
Score: 37.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 52.96% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX519039 (1-41)

Qy 3 ProProValGluLysLeuLeuProLeu 11
Db 33 CCACCTGTGGAGMCTTTCCTACCATG 7

RESULT 3
LOCUS CQ001968 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 608 from Patent WO0147944.
ACCESSION CQ001968
VERSION CQ001968.1 GI:41008600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 608 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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ORIGIN

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Best Local Similarity: 81.82% Mismatches: 1
Query Match: 65.71% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX093019 (1-43)

Qy 1 SerAsnProValGluLysLeuLeuProLeu 11
Db 38 TCGAACCCCTCCGTGAAGGCCCTTCTACCATTA 6

RESULT 2
LOCUS AX519039/c 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5237 from Patent WO02052044.
ACCESSION AX519039
VERSION AX519039.1 GI:23569098
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5237 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 381 Length: 41
Score: 37.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 52.96% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX519039 (1-41)

Qy 3 ProProValGluLysLeuLeuProLeu 11
Db 33 CCACCTGTGGAGMCTTTCCTACCATG 7

RESULT 3
LOCUS CQ001968 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 608 from Patent WO0147944.
ACCESSION CQ001968
VERSION CQ001968.1 GI:41008600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 608 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43927434"

ORIGIN

Alignment Scores:
Pred. No.: 709 Length: 51
Score: 36.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 51.43% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CQ001968 (1-51)

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Db 1 AGCAGGCTCTAGTCGCTCGCTTAATTACCGTGACITTA 39

RESULT 4
LOCUS A24246 39 bp DNA linear PAT 04-DEC-1994
DEFINITION Oligonucleotide.
ACCESSION A24246
VERSION A24246.1 GI:833653
KEYWORDS Rattus rattus (black rat)
SOURCE Rattus rattus
ORGANISM Rattus rattus
REFERENCE 1
AUTHORS HUMANIZED INTERLEUKIN-2 RECEPTORS ANTIBODIES
TITLE Patent: WO 9301289-A 30 21-JAN-1993;
JOURNAL Location/Qualifiers
FEATURES
source 1..39
/organism="Rattus rattus"
/mol_type="unassigned DNA"
/db_xref="taxon:10117"

ORIGIN

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Pred. No.: 677 Length: 39
Score: 35.50 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 50.71% Indels: 1
DB: 6 Gaps: 1

US-09-980-881A-9 (1-14) x A24246 (1-39)

Qy 3 ProProValGluLysLeuLeuProLeuSerLeuLys 14
Db 5 CCCCCTGGTG---AAGCTGTACTCTTGTGCACAGAA 37

RESULT 5
LOCUS CQ767550 45 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 17 from Patent EP1386931.
ACCESSION CQ767550
VERSION CQ767550.1 GI:45095665
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1
AUTHORS Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
TITLE Human neurotrophin homologue
JOURNAL Patent: EP 1386931-A 17 04-FEB-2004;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

ORIGIN
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Alignment Scores:  
Pred. No.: 953 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CQ767550 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
DB 32 AGCAATGCCCGGTTCAGGCGTCTCCCC 3

RESULT 6

LOCUS AX201424/c 45 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 103 from Patent WO0153486.  
ACCESSION AX201424  
VERSION AX201424.1 GI:15391230

KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V., Stone, D.W., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of tumour  
JOURNAL Patent: WO 0153486-A 103 26-JUL-2001;  
Genentech, Inc. (US)

FEATURES  
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Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic Oligonucleotide Probe."

ORIGIN

Alignment Scores:  
Pred. No.: 953 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX201424 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
DB 32 AGCAATGCCCGGTTCAGGCGTCTCCCC 3

RESULT 7

LOCUS AR364159 34 bp DNA linear PAT 03-SEP-2003  
DEFINITION Sequence 42 from patent US 5256545.  
ACCESSION AR364159  
VERSION AR364159.1 GI:34426485

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Brown, M.S., Goldstein, J.L., Russell, D.W. and Sudhof, T.C.  
TITLE Sterol Regulatory Elements  
JOURNAL Patent: US 5256545-A 42 26-OCT-1993;  
FEATURES Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1,11e+03 Length: 34  
Score: 34.00 Matches: 7  
Percent Similarity: 70.00% Conservative: 0  
Best Local Similarity: 70.00% Mismatches: 3  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR364159 (1-34)

QY 2 AsnProValGluLysLeuLeuProLeu 11  
DB 4 AATCACCCCACTGCAAAACTCTCCCTCG 33

RESULT 8

LOCUS AR053703 40 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 127 from patent US 5834252.  
ACCESSION AR053703  
VERSION AR053703.1 GI:5978565

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 40)  
AUTHORS Stemmer, W.Peter, Christiaan, and Lipshutz, R.J.  
TITLE End-complementary polymerase reaction  
JOURNAL Patent: US 5834252-A 127 10-NOV-1998;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1,29e+03 Length: 40  
Score: 34.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 1  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR053703 (1-40)

QY 3 ProProValGluLysLeuLeuProLeuSer 12  
DB 3 CCGCCTTGTGAGTGAGCTGATACGCTCGCC 32

RESULT 9

LOCUS AR258638 40 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 127 from patent US 6489146.  
ACCESSION AR258638  
VERSION AR258638.1 GI:27309014

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 40)  
AUTHORS Stemmer, W.P.C. and Lipshutz, R.J.  
TITLE End-complementary polymerase reaction  
JOURNAL Patent: US 6489146-A 127 03-DEC-2002;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1,29e+03 Length: 40  
Score: 34.00 Matches: 5  
Percent Similarity: 90.00% Conservative: 4









GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 01:58:08 ; Search time 85 Seconds  
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Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
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Fgapop 10.0 , Fgapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 934402

Minimum DB seq length: 0  
Maximum DB seq length: 57  
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Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	48.6	34	6	Patent No. 5256545
2	34	48.6	40	2	US-08-425-684-127
3	34	48.6	40	2	US-08-675-502-127
4	34	48.6	40	4	US-09-245-802-127
5	34	48.6	41	1	US-08-168-917-16
6	34	48.6	41	2	US-08-460-510-16
7	34	48.6	41	2	US-08-460-490-16
8	34	48.6	41	5	PCT-US92-00730-16
9	34	48.6	41	5	PCT-US92-10430-11
10	34	48.6	51	2	US-08-350-260A-287
11	34	48.6	51	4	US-09-104-337A-287
12	33	47.1	36	2	US-08-816-155B-38

13	33	47.1	36	3	US-08-815-809-23	Sequence 23, Appl
14	33	47.1	36	3	US-09-079-587-38	Sequence 38, Appl
C 15	33	47.1	41	1	US-08-168-917-18	Sequence 18, Appl
C 16	33	47.1	41	2	US-08-460-510-18	Sequence 18, Appl
C 17	33	47.1	41	2	US-08-460-490-18	Sequence 18, Appl
C 18	33	47.1	41	5	PCT-US92-00730-18	Sequence 18, Appl
19	33	47.1	41	5	PCT-US92-10430-13	Sequence 13, Appl
20	32	45.7	33	4	US-09-566-420-2	Sequence 2, Appl
C 21	32	45.7	33	4	US-10-201-764-2	Sequence 2745, Ap
C 22	32	45.7	47	4	US-09-422-978-2745	Sequence 2745, Ap
23	32	45.7	54	1	US-08-373-124A-2192	Sequence 2192, Ap
C 24	32	45.7	54	1	US-08-435-628-2192	Sequence 2192, Ap
C 25	31	44.3	43	3	US-08-832-985-52	Sequence 52, Appl
C 26	31	44.3	43	4	US-09-410-903-33	Sequence 33, Appl
C 27	31	44.3	43	4	US-08-835-159-52	Sequence 52, Appl
C 28	31	44.3	47	1	US-08-093-884-31	Sequence 31, Appl
C 29	30	42.9	39	4	US-09-548-797B-151	Sequence 151, Appl
30	30	42.9	39	4	US-09-548-797B-152	Sequence 152, Appl
C 31	30	42.9	45	2	US-08-494-151-2	Sequence 2, Appl
C 32	30	42.9	47	4	US-09-422-978-522	Sequence 2273, Ap
C 33	30	42.9	47	4	US-09-422-978-522	Sequence 2273, Ap
C 34	30	42.9	50	2	US-08-709-368-2	Sequence 2, Appl
C 35	30	42.9	52	4	US-08-956-171B-2252	Sequence 2252, Ap
C 36	30	42.9	52	4	US-08-781-986A-2252	Sequence 2252, Ap
C 37	30	42.9	54	1	US-08-366-953A-23	Sequence 23, Appl
C 38	30	42.9	54	1	US-08-311-486C-1099	Sequence 1099, Ap
C 39	30	42.9	56	4	US-09-270-767-29728	Sequence 29728, A
C 40	29.5	42.1	44	3	US-08-865-960-9	Sequence 9, Appl
C 41	29.5	42.1	55	2	US-08-850-049-70	Sequence 70, Appl
C 42	29.5	42.1	55	2	US-08-850-049-71	Sequence 71, Appl
C 43	29.5	42.1	55	2	US-08-850-049-74	Sequence 74, Appl
C 44	29.5	42.1	55	2	US-08-050-478-70	Sequence 70, Appl
C 45	29.5	42.1	55	2	US-08-050-478-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
5256545-42  
; Patent No. 5256545  
; APPLICANT: BROWN, MICHAEL S.; GOLDSTEIN, JOSEPH L.; RUSSELL,  
; DAVID W.; SUDHOF, THOMAS C.  
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/425,852  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 33,330  
; FILING DATE: 30-MAR-1987  
; APPLICATION NUMBER: 33,081  
; FILING DATE: 30-MAR-1987  
; SEQ ID NO:42:  
; LENGTH: 34  
5256545-42

Alignment Scores:  
Pred. No.: 61.2 Length: 34  
Score: 34.00 Matches: 7  
Percent Similarity: 70.00% Conservative: 0  
Best Local Similarity: 70.00% Mismatches: 3  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x 5256545-42 (1-34)

Qy 2 AsnProValGluLysLeuLeuProLeu 11

Db 4 AATCACCCTACTGCATAACTCTCTCCCCCTG 33

RESULT 2  
US-08-425-684-127  
; Sequence 127, Application US/08425684

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; Patent No. 5834252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN ESO., TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528J-015400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-425-684-127

Alignment Scores:
Pred. No.: 75.3 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-425-684-127 (1-40)

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US-08-675-502-127
; Sequence 127, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US/08/675,502

US-09-980-881A-9 (1-14) x US-08-675-502-127 (1-40)

Qy 3 ProProValGlulysLeuLeuProLeuSer 12
|||...: :|||...:|
Db 3 CCGCCTTGAGTGAGCTGATACCGCTGCC 32

RESULT 4
US-09-245-802-127
; Sequence 127, Application US/09245802
; Patent No. 6489146
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US/09/245,802
```

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; NAME: MURPHY, ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
;
; Alignment Scores:
; Pred. No.: 75.3 Length: 40
; Score: 34.00 Matches: 5
; Percent Similarity: 90.00% Conservative: 4
; Best Local Similarity: 50.00% Mismatches: 1
; Query Match: 48.57% Indels: 0
; DB: 4 Gaps: 0
;
US-09-980-881A-9 (1-14) x US-09-245-802-127 (1-40)
;
Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32
;
RESULT 5
US-08-168-917-16/c
; Sequence 16, Application US/08168917
; Patent No. 5686572
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
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```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-168-917-16
;
; Alignment Scores:
; Pred. No.: 77.7 Length: 41
; Score: 34.00 Matches: 6
; Percent Similarity: 100.00% Conservative: 2
; Best Local Similarity: 75.00% Mismatches: 0
; Query Match: 48.57% Indels: 0
; DB: 1 Gaps: 0
;
US-09-980-881A-9 (1-14) x US-08-168-917-16 (1-41)
;
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAATT 14
;
RESULT 6
US-08-460-510-16/c
; Sequence 16, Application US/08460510
; Patent No. 5872218
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; STREET: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,510
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
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US-08-460-510-16

Alignment Scores: 77.7 Length: 41  
Pred. No.: 34.00 Matches: 6  
Score: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-460-510-16 (1-41)

Qy 1 SerAsnProValGluLysLeu 8  
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 7

US-08-460-490-16/c

; Sequence 16, Application US/08460490

; Patent No. 5891652

; GENERAL INFORMATION:

; APPLICANT: Wolf, David

; APPLICANT: Tomlinson, James E.

; APPLICANT: Fretto, Larry J.

; APPLICANT: Giese, Neill A.

; APPLICANT: Escobedo, Jaime A.

; APPLICANT: Williams, Lewis T.

; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and CREW

; STREET: One Market Plaza, Stuart Street Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,490

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684

; REFERENCE/DOCKET NUMBER: 012418-001420

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 41 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo Sapiens

; STRAIN: lambda gt10

US-08-460-490-16

Alignment Scores: 77.7 Length: 41  
Pred. No.: 34.00 Matches: 6  
Score: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0

DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-460-490-16 (1-41)

Qy 1 SerAsnProValGluLysLeu 8  
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 8

PCT-US92-00730-16/c

; Sequence 16, Application PC/TUS9200730

; GENERAL INFORMATION:

; APPLICANT: Wolf, David

; APPLICANT: Tomlinson, James E.

; APPLICANT: Fretto, Larry J.

; APPLICANT: Giese, Neill A.

; APPLICANT: Escobedo, Jaime A.

; APPLICANT: Williams, Lewis T.

; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND

; STREET: Stuart Street Tower, 20th Floor \ One Market

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00730

; FILING DATE: 19920128

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: 12418-14

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 41 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo Sapiens

; STRAIN: lambda gt10

PCT-US92-00730-16

Alignment Scores: 77.7 Length: 41  
Pred. No.: 34.00 Matches: 6  
Score: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 5 Gaps: 0

US-09-980-881A-9 (1-14) x PCT-US92-00730-16 (1-41)

Qy 1 SerAsnProValGluLysLeu 8  
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 9  
PCT-US92-10430-11  
; Sequence 11, Application PC/TUS9210430  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; ADDRESSEE: Wolf, David  
; TITLE OF INVENTION: Methods for Production of Purified  
; TITLE OF INVENTION: Soluble Type B and Type A Human Platelet-Derived Growth  
; TITLE OF INVENTION: Factor Receptor Fragments  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10430  
; FILING DATE: 19921201  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,794  
; FILING DATE: 02-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 12418-15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US92-10430-11  
Alignment Scores:  
Pred. No.: 77.7 Length: 41  
Score: 34.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 5 Gaps: 0  
US-09-980-881A-9 (1-14) x PCT-US92-10430-11 (1-41)  
Qy 1 SerAsnProValGluLysLeu 8  
|||||  
Db 5 TCGAATCGGCAGTTAGGAACTT 28  
RESULT 10  
US-08-350-260A-287  
; Sequence 287, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 287:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-350-260A-287  
Alignment Scores:  
Pred. No.: 103 Length: 51  
Score: 34.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 48.57% Indels: 0  
DB: 2 Gaps: 0  
US-09-980-881A-9 (1-14) x US-08-350-260A-287 (1-51)  
Qy 3 ProProValGluLysLeuProLeu 11  
|||||  
Db 11 CGCCGGAATACGAAGTTGCTCCACTG 37  
RESULT 11  
US-09-104-337A-287  
; Sequence 287, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul

Griffiths, Andrew David  
Williams, Samuel Cameron  
Waterhouse, Peter  
Nissim, Ahuva  
Johnson, Kevin Stuart  
Smith, Andrew John Hammond  
TITLE OF INVENTION: Methods for producing members of specific  
binding pairs  
NUMBER OF SEQUENCES: 600  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Audrey L. Bartnicki  
STREET: Marshall, Gerstein & Borun  
6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/104,337A  
FILING DATE: 25-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/350,260  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
APPLICATION NUMBER: PCT/GB93/00605  
FILING DATE: 24-MAR-1993  
APPLICATION NUMBER: US 08/150,002  
FILING DATE: 31-MAR-1994  
APPLICATION NUMBER: US 08/307,619  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bartnicki, Audrey L.  
REGISTRATION NUMBER: 40,499  
REFERENCE/DOCKET NUMBER: 28111/32372A  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 287:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 287:  
US-09-104-337A-287  
Alignment Scores:  
Pred. No.: 103 Length: 51  
Score: 34.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 48.57% Indels: 0  
DB: 4 Gaps: 0  
US-09-980-881A-9 (1-14) x US-09-104-337A-287 (1-51)  
Qy 3 ProProValGluLysLeuProLeu 11  
Db 11 CGCGCAATACGAGTGTGCTCCACTG 37  
RESULT 12  
US-08-816-155B-38  
Sequence 38, Application US/08816155B  
Patent No. 5990091

GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,155B  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2950  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-816-155B-38  
Alignment Scores:  
Pred. No.: 101 Length: 36  
Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 2 Gaps: 0  
US-09-980-881A-9 (1-14) x US-08-816-155B-38 (1-36)  
Qy 3 ProProValGluLysLeuPro 10  
Db 1 CCCCCGCGAGAAATTAAGGCC 24  
RESULT 13  
US-08-815-809-23  
Sequence 23, Application US/08815809  
Patent No. 6004777  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, James  
APPLICANT: GOEBEL, Scott J.  
APPLICANT: COX, William I.  
APPLICANT: GETTIG, Russell R.  
APPLICANT: PINCUS, Steven E.  
APPLICANT: PAOLETTI, Enzo  
APPLICANT: JACOBS, Bertram L.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF  
MAKING AND USES THEREOF  
FILE REFERENCE: 454310-3010  
CURRENT APPLICATION NUMBER: US/08/815,809  
CURRENT FILING DATE: 1997-03-12

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 36  
; TYPE: DNA  
; ORGANISM: Vaccinia virus  
US-08-815-809-23

Alignment Scores:  
Pred. No.: 101 Length: 36  
Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-815-809-23 (1-36)

Qy 3 ProProValGlulysLeuLeuPro 10  
Db 1 CCCCCTGCAGAAAAATTAGGCC 24

## RESULT 14

US-09-079-587-38  
; Sequence 38, Application US/09079587  
; Patent No. 6130066  
; GENERAL INFORMATION:  
; APPLICANT: TARTAGLIA, JAMES  
; APPLICANT: COX, WILLIAM I.  
; APPLICANT: GETTIG, RUSSELL R.  
; APPLICANT: MARTINEZ, HECTOR  
; APPLICANT: PAOLETTI, ENZO  
; APPLICANT: PINCUS, STEVEN E.  
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
; METHODS OF MAKING AND USES THEREOF  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
; STREET: 745 FIFTH AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10151

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,587  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/816,155  
; FILING DATE: 12-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOWALSKI, THOMAS J.  
; REGISTRATION NUMBER: 32,147  
; REFERENCE/DOCKET NUMBER: 454310-2990  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-588-0800  
; TELEFAX: 212-588-0500  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-09-079-587-38  
Alignment Scores:  
Pred. No.: 101 Length: 36  
Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 3 Gaps: 0

Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-079-587-38 (1-36)

Qy 3 ProProValGlulysLeuLeuPro 10  
Db 1 CCCCCTGCAGAAAAATTAGGCC 24

## RESULT 15

US-08-168-917-18/c  
; Sequence 18, Application US/08168917  
; Patent No. 5686572  
; GENERAL INFORMATION:  
; APPLICANT: Wolf, David  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Fretto, Larry J.  
; APPLICANT: Giese, Neill A.  
; APPLICANT: Escobedo, Jaime A.  
; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
; PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND  
; STREET: Steuart Street Tower, 20th Floor \ One Market  
; STREET: Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,917  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/650,793  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: 12418-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapiens  
; STRAIN: lambda gt10

US-08-168-917-18  
Alignment Scores:  
Pred. No.: 119 Length: 41  
Score: 33.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 47.14% Indels: 0

DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-18 (1-41)

Qy 1 SerAsnProProValGluLysLeuLeu 9

|||||

Db 37 TCGAATCCGCCAGTTATGATGTTGCTT 11

Search completed: October 31, 2004, 03:42:04  
Job time : 88 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 03:01:14 ; Search time 366 Seconds  
(without alignments)  
196.138 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 197578

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USFPO\_spool/US0980881/runat\_28102004.131505.11506/app.query.fasta\_1.199  
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=57 -USER=US0980881 @CNG 1.1 480 @runat\_28102004.131505.11506 -NCPU=6  
-ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database : Published Applications NA: \*  
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6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq: \*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq: \*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq: \*  
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10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq: \*  
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13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq: \*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq: \*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq: \*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq: \*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq: \*  
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: \*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq: \*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq: \*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\*

Result No.	Score	Query Match	Length	DB ID	Description
C 1	46	65.7	43	10	US-09-845-064-24
C 2	37	52.9	41	16	US-10-035-833A-5237
C 3	35	50.0	45	9	US-09-978-295A-17
C 4	35	50.0	45	9	US-09-978-697-17
C 5	35	50.0	45	9	US-09-978-192A-17
C 6	35	50.0	45	9	US-09-999-832A-17
C 7	35	50.0	45	10	US-09-978-189-17
C 8	35	50.0	45	10	US-09-978-608A-17
C 9	35	50.0	45	10	US-09-978-585A-17
C 10	35	50.0	45	10	US-09-978-191A-17
C 11	35	50.0	45	10	US-09-978-403A-17
C 12	35	50.0	45	10	US-09-978-564A-17
C 13	35	50.0	45	10	US-09-999-833A-17
C 14	35	50.0	45	10	US-09-981-915A-17
C 15	35	50.0	45	10	US-09-978-824-17
C 16	35	50.0	45	10	US-09-918-585A-17
C 17	35	50.0	45	10	US-09-999-834A-17
C 18	35	50.0	45	10	US-09-978-423A-17
C 19	35	50.0	45	10	US-09-978-193A-17
C 20	35	50.0	45	10	US-09-999-830A-17
C 21	35	50.0	45	10	US-09-978-757A-17
C 22	35	50.0	45	10	US-09-978-187B-17
C 23	35	50.0	45	10	US-09-978-643A-17
C 24	35	50.0	45	10	US-09-978-375A-17
C 25	35	50.0	45	10	US-09-978-298A-17
C 26	35	50.0	45	10	US-09-978-188A-17
C 27	35	50.0	45	10	US-09-978-681A-17
C 28	35	50.0	45	10	US-09-978-194A-17
C 29	35	50.0	45	10	US-09-999-829A-17
C 30	35	50.0	45	10	US-09-978-299A-17
C 31	35	50.0	45	10	US-09-978-544A-17
C 32	35	50.0	45	10	US-09-978-665A-17
C 33	35	50.0	45	10	US-09-978-802A-17
C 34	35	50.0	45	11	US-09-999-831A-17
C 35	35	50.0	45	14	US-10-017-081A-17
C 36	35	50.0	45	14	US-10-167-749-17
C 37	35	50.0	45	14	US-10-013-921A-17
C 38	35	50.0	45	14	US-10-013-922A-17
C 39	35	50.0	45	14	US-10-016-177A-17
C 40	35	50.0	45	15	US-10-166-709A-17
C 41	35	50.0	45	15	US-10-143-031A-17
C 42	35	50.0	45	15	US-10-143-030A-17
C 43	35	50.0	45	15	US-10-002-967A-17
C 44	35	50.0	45	15	US-10-017-083A-17
C 45	35	50.0	45	15	US-10-145-128A-17

ALIGNMENTS

RESULT 1  
US-09-845-064-24/c  
; Sequence 24, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845, 064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Oligo  
; OTHER INFORMATION: Desoxynucleotide containing StuI restriction site

## US-09-845-064-24

Alignment Scores:  
Pred. No.: 4.15 Length: 43  
Score: 46.00 Matches: 9  
Percent Similarity: 90.91% Conservative: 1  
Best Local Similarity: 81.82% Mismatches: 1  
Query Match: 65.71% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-845-064-24 (1-43)

Qy 1 SerhsnProValGluLysLeuLeuProLeu 11  
Db 38 TCGAACCCCTCCGGAAGGCCCTTCTACCATTA 6

## RESULT 2

US-10-035-833A-5237/C  
; Sequence 5237, Application US/10035833A  
; Publication No. US20040072156A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yuho  
; APPLICANT: Sekine, Akihiro  
; APPLICANT: Iida, Aritoshi  
; APPLICANT: Saito, Osamu  
; TITLE OF INVENTION: Detection of Genetic Polymorphisms  
; FILE REFERENCE: FORS-06904  
; CURRENT APPLICATION NUMBER: US/10/035.833A  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 7669  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5237  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-035-833A-5237

Alignment Scores:  
Pred. No.: 153 Length: 41  
Score: 37.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 52.86% Indels: 0  
DB: 16 Gaps: 0

US-09-980-881A-9 (1-14) x US-10-035-833A-5237 (1-41)

Qy 3 ProProValGluLysLeuLeuProLeu 11  
Db 33 CCACCTGTGGAGMCTTCTTCTACCACTG 7

## RESULT 3

US-09-978-295A-17/C  
; Sequence 17, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
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; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637

; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
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; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	9	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-978-295A-17 (1-45)

Qy 1 SerAsnProProValGlulysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAAGCCCTGCTCCCC 3

## RESULT 4

US-09-978-697-17/c  
; Sequence 17, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Pong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
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## RESULT 5

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC9  
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-999-832A-17 (1-45)

Qy 1 SerAsnProProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCGTCTGCC 3

RESULT 7
US-09-978-189-17/c
; Sequence 17, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR FILING DATE: 1998-03-26
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; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
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; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
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; PRIOR FILING DATE: 1998-04-29  
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; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-5-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
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; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-189-17 (1-45)

Qy 1 SerAsnProValGlulysLeuLeuPro 10  
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Db 32 AGCAATGCCCGGTTCAAGGCGCTGCTCCCC 3

RESULT 8  
US-09-978-608A-17/c  
; Sequence 17, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978.608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-608A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-608A-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 9
US-09-978-585A-17/c
; Sequence 17, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-585A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-585A-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCCTGCTCCCC 3

RESULT 10
US-09-978-191A-17/c
; Sequence 17, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083366	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697	PRIOR FILING DATE: 1998-05-15

Alignment Scores: 45  
Pred. No.: 382 Length: 7  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservatives: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881a-9 (1-14) x US-09-978-191a-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAGGCGCTGCTCCC 3

#### RESULT 11

US-09-978-403A-17/c

Sequence 17, Application US/09978403A

Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
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Db 32 AGCATGCCCCGGTTCAAGCCCTGCTCCCC 3
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; Sequence 17, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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66	PRIOR FILING DATE: 1998-05-15	
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Alignment Scores:

Pred. No.:

382

Length:

45

**Score:**

35.00

**Matches:**

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Percent Similarity: 80.00%      Conservative: 1  
Best Local Similarity: 70.00%      Mismatches: 2  
Query Match: 50.00%      Indels: 0  
DB: 10      Gaps: 0

US-09-980-881a-9 (1-14) x US-09-978-564A-17 (1-45)

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Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

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US-09-999-833A-17/c

; Sequence 17, Application US/09999833A

; Publication No. US20030054405A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerbet, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C65

; CURRENT APPLICATION NUMBER: US/09/999,833A

; CURRENT FILING DATE: 2001-10-24

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; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Length: 45  
Matches: 7  
Conservative: 1  
Mismatch: 2

Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-980-881A-9 (1-14) x US-09-999-833A-17 (1-45)  
Qy 1 SerAsnProValGluLysLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGCGCTGCTCC 3  
RESULT 14  
US-09-981-915A-17/c  
; Sequence 17, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Daniel  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C12  
; CURRENT APPLICATION NUMBER: US/09/981,915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910



; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
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; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-27  
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; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
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; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881a-9 (1-14) x US-09-981-915A-17 (1-45)

Qy 1 SerAnProValGluLysLeuLeuPro 10  
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Db 32 AGCAATGCCCGTTCAGGCGTCTCCCC 3

## RESULT 15

US-09-978-824-17/c

; Sequence 17, Application US/09978824

; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C14

; CURRENT FILING DATE: 2001-10-17

; PRIOR FILING DATE: 2001-07-30

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/079656

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; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079689

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; PRIOR FILING DATE: 1998-03-31

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; PRIOR FILING DATE: 1998-04-23

; PRIOR APPLICATION NUMBER: 60/083336

; PRIOR FILING DATE: 1998-04-27

1 PRIOR APPLICATION NUMBER: 60/083322  
2 PRIOR FILING DATE: 1998-04-28  
3 PRIOR APPLICATION NUMBER: 60/083392  
4 PRIOR FILING DATE: 1998-04-29  
5 PRIOR APPLICATION NUMBER: 60/083495  
6 PRIOR FILING DATE: 1998-04-29  
7 PRIOR APPLICATION NUMBER: 60/083496  
8 PRIOR FILING DATE: 1998-04-29  
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20 PRIOR FILING DATE: 1998-04-29  
21 PRIOR APPLICATION NUMBER: 60/083742  
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23 PRIOR APPLICATION NUMBER: 60/084366  
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25 PRIOR APPLICATION NUMBER: 60/084414  
26 PRIOR FILING DATE: 1998-05-06  
27 PRIOR APPLICATION NUMBER: 60/084441  
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31 PRIOR APPLICATION NUMBER: 60/084639  
32 PRIOR FILING DATE: 1998-05-07  
33 PRIOR APPLICATION NUMBER: 60/084640  
34 PRIOR FILING DATE: 1998-05-07  
35 PRIOR APPLICATION NUMBER: 60/084598  
36 PRIOR FILING DATE: 1998-05-07  
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38 PRIOR FILING DATE: 1998-05-07  
39 PRIOR APPLICATION NUMBER: 60/084627  
40 PRIOR FILING DATE: 1998-05-07  
41 PRIOR APPLICATION NUMBER: 60/084643  
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43 PRIOR APPLICATION NUMBER: 60/085339  
44 PRIOR FILING DATE: 1998-05-13  
45 PRIOR APPLICATION NUMBER: 60/085338  
46 PRIOR FILING DATE: 1998-05-13  
47 PRIOR APPLICATION NUMBER: 60/085323  
48 PRIOR FILING DATE: 1998-05-13  
49 PRIOR APPLICATION NUMBER: 60/085582  
50 PRIOR FILING DATE: 1998-05-15  
51 PRIOR APPLICATION NUMBER: 60/085700  
52 PRIOR FILING DATE: 1998-05-15  
53 PRIOR APPLICATION NUMBER: 60/085689  
54 PRIOR FILING DATE: 1998-05-15  
55 PRIOR APPLICATION NUMBER: 60/085579  
56 PRIOR FILING DATE: 1998-05-15  
57 PRIOR APPLICATION NUMBER: 60/085580  
58 PRIOR FILING DATE: 1998-05-15  
59 PRIOR APPLICATION NUMBER: 60/085573  
60 PRIOR FILING DATE: 1998-05-15  
61 PRIOR APPLICATION NUMBER: 60/085704  
62 PRIOR FILING DATE: 1998-05-15  
63 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-824-17 (1-45)

Qy 1 SerAsnProProValGluLysLeuLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGCGCTGCTCCCC 3

Search completed: October 31, 2004, 04:34:55  
Job time : 370 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 28, 2004, 18:47:56 ; Search time 44.5 Seconds  
(without alignments)  
4688.459 Million cell updates/sec

Title: US-09-980-881A-1

Perfect score: 2777

Sequence: 1 agaaaattgtgtggatg.....aaaaaaaaaaaaaaaaaaaa 1573

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlip  
-Q=/cgn2\_1/USFTO\_spool\_p/US09980881/runat\_28102004\_131901\_29505/app\_query.fasta\_1.1735  
-DB=issued Patents AA -QFMT=faстан -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09980881 @CGN 1.1.46 @runat\_28102004\_131901\_29505 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PGTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1902.5	68.5	386	4	US-09-813-133A-2
2	1885	67.9	423	1	Sequence 2, Appli
3	1885	67.9	423	1	Sequence 3, Appli
4	1885	67.9	423	1	Sequence 3, Appli
5	1885	67.9	423	2	Sequence 2, Appli
6	1874	67.5	423	4	US-08-869-057-2
7	655	23.6	417	1	US-09-813-133A-4
8	655	23.6	417	1	US-07-649-591B-7
9	655	23.6	417	1	US-08-277-540-7
10	651.5	23.5	415	2	US-08-430-787A-7
11	651.5	23.5	415	4	US-08-860-882A-57
12	647.5	23.3	417	1	US-09-011-769A-39
					Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-2

; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Alignment Scores: 3.68e-202 Length: 386  
Pred. No.: 1902.50 Matches: 363  
Score: 94.30% Conservative: 1  
Percent Similarity: 94.30% Mismatches: 5  
Best Local Similarity: 94.04% Indels: 18  
Query Match: 68.51% Gaps: 1  
DB: 4

US-09-980-881A-1 (1-1573) x US-09-813-133A-2 (1-386)

QY 18 ATGAAGCTTTCAGACCTTCAGTCCCTGTGACCATTTCTCTCTGTGAGCAGCATGTC 77  
|||||  
Db 1 MetLysLeuCySerLeuAlaValLeuValProIleValLeuPheCy6GluGlnHisVal 20  
|||||  
QY 78 TTGCGGCTTCAGATGGCCAAAGTTCTAGCTGCTTCTTCTTAGAACCTCTTAGGCAAGTTCAA 137  
|||||

Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Qy GTTCTACAGATCTTACTCAACATATGAGATTTCTCTGGCAGCGGTAAACAGCTGAC 197  
Db 41 ValLeuGlnSerLeuThrThrThrTyGluLeuValLeuTrpGlnProValThrAlaAsp 60  
Qy CTTATTGTGAAGAAAAAAGTCCATTTTGTAAATGATCATGTGTCGCAATGTG 257  
Db 61 LeuileVallyslsGlnValHisPheValAsnAlaSerAspValAspVal 80  
Qy AAAGCCCATTTAAATGTCAGGGAAATCCATGTCAGTCTCTGTCGAGAGCTGGAAT 317  
Db 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
Qy CTTATTCAACAGCAGATTTTCAACACACACAGTCCGCGAGCTCCGATCGTACTAT 377  
Db 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyThr 120  
Qy GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGCAT 437  
Db 121 GluGlnTyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArgHis 140  
Qy CCTGATATGCTTCAAAAATCCACATTTGGATCCCTCATTTGAGAGTACCCTCTATGTT 497  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyVal 160  
Qy TTTAAAGGTTCTGGAAGAAGCAACACAGCCCAAAATGCCATATGATTTGGAATC 557  
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyLe 180  
Qy CATGCCAGAGATGGATCTCTCTGCTTCTGCTTCTGCTTGGTTTCATAGGCCATATCGAATG 617  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Qy TGGAGAAGACCTCTTCTTATGCGCAACATCATTTGCATCGCAACAGACCTGAATAGC 677  
Db 201 TrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220  
Qy AACTTTGCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGAAACC 737  
Db 221 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
Qy TACTGTGACCTTATCTGAGTCAGAACAGACAGAGTGAAGCGAGTGGCTAGTTCTTGAGA 797  
Db 241 TyrCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Qy AGAATATCAACAGATTAAGACATACATCAGCATGATTCATATCCAGCATATAGTG 857  
Db 261 ArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHisIleVal 280  
Qy TTTCATATTCCTATACACGAAGTAAAGCAACACCATGAGGAACCTGCTCTAGTAGCC 917  
Db 281 PheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
Qy AGTGAAGCAGTTCTGCTATTGACAAACTAGTAAATAATACAGGTATACATGCGCAT 977  
Db 301 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyThrHisGlyHis 320  
Qy GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTCGATCTATGATTTGGGC 1037  
Db 321 GlySerGluThrLeuTyLeuAlaProGlyGlyAspAspTrpIleTyAspLeuGly 340  
Qy ATCAAAATATTCGTT----- 1051  
Db 341 IleLysTySerPheThrIleGluLeuArgAspThrGlyThrTyGlyPheLeuLeuPro 360  
Qy 1052 -----TACATCAACCCACCTGTAGACAGCTTTTCCGCTGTCTTAAATAGCTGG 1105  
Db 361 GluArgTyIleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrp 380  
Qy 1106 CATGTCATTAGGAATGTT 1123  
Db 381 HisValIleArgAsnVal 386

## RESULT 2

US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-649-591B-3

Alignment Scores: 3,37e-200 Length: 423  
Pred. No.: 1885.00 Matches: 365  
Score: 1885.00  
Percent Similarity: 86.52% Conservative: 1  
Best Local Similarity: 86.29% Mismatches: 3  
Query Match: 67.88% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-1 (1-1573) x US-07-649-591B-3 (1-423)

Qy 18 ATGAAGCTTTGACAGCTTGCAGTCTTGATCCCATTTGTTCTTCTGTGAGCAGCATGTC 77  
Db 1 MetCysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Qy 78 TTCGCGTTCCAGAGTGGCCAAAGTTCTAGTGTCTTCTTCTAGAACCTCTAGGCAAGTTCAA 137  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Qy 138 GTTCTACAGATCTTACTACACATATGATTTGTTCTCTGCGAGCGGTAAACAGCTGAC 197  
Db 41 ValLeuGlnAsnLeuThrThrThrTyGluLeuValLeuTrpGlnProValThrAlaAsp 60  
Qy 198 CTTATTGTGAAGAAAAAAGTCCATTTTGTAAATGCATCTATGTGCGCAATGTG 257  
Db 61 LeuileVallyslsLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Qy 258 AAAGCCCATTTAAATGTGAGCGGAATTCATGAGTGTCTTGTGCGAGAGCTGGAAGAT 317  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100



QY 318 CTTATTCAACGACAGATTTCACAGCACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT 377  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyr 120  
QY 378 GAACAGTATCACTCACATAAATGAATCTATTCTTGGATAGATTTATAACTTGAGAGGCAT 437  
Db 121 GluGlnIyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
QY 438 CCGTATATGCTTACAAAAATCCACATTCGATCCCTCATTTGAGAAGTACCCCACTCTATGTT 497  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
QY 498 TTAAGGTTTCTGAAAAAGACAAACAGACCCAAAAATCCATATGATGATCTGAGGATC 557  
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
QY 558 CATCCAGAGAATCGATCTCTCCGCTTCTCGCTTGTGTTGTTTCATAGGCCAT----- 608  
Db 181 HisAlaArgGluIleTrpIleSerProAlaPheCysLeuIleTrpPheIleGlyHisIleThrGln 200  
QY 608 ----- 608  
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220  
QY 609 -----AATCGAATGTGGAGAAAG 626  
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240  
QY 627 AACGGTTCTTCTATGCGAACAAATCATTGTCATCGACAGACCTGAATAGCACTTTGTC 686  
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
QY 687 TCCAAACACTGGTGTGAGGAGGTGCATCCAGTTCTCTATGCTCGGAAACCTACTGTGGA 746  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280  
QY 747 CTTTATCTAGTCAGAACACAGAGTGAAGCAGTGGCTAGTTCTTTGAGAAGAAATATC 806  
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300  
QY 807 AACGAGATTAAGCATACATCAGCATGCATTCTACTCCAGCATATAGTGTTCATAT 866  
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320  
QY 867 TCCTATACAGAACTAAAGCAAAAGACCATGAGGAAGTCTCTAGTAGCCAGTGAAGCA 926  
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340  
QY 927 GTTCGTCTATTGACAAACTAGTAAANAATACCAAGGTATACACATGGCCATGGCTCAGAA 986  
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360  
QY 987 ACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAATAT 1046  
Db 361 ThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyrAspLeuGlyIleLysTyr 380  
QY 1047 TCGTT-----TAC 1054  
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400  
QY 1055 ATCAACCCACCTGTAGAGAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGTCTATT 1114  
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrpHisValIle 420  
QY 1115 AGGAATGTT 1123  
Db 421 ArgAsnVal 423

RESULT 4  
US-08-430-787A-3  
; Sequence 3, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:

APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1CID1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-3  
Alignment Scores:  
Pred. No.: 3,37e-200 Length: 423  
Score: 1885.00 Matches: 365  
Percent Similarity: 86.52% Conservative: 1  
Best Local Similarity: 86.29% Mismatches: 3  
Query Match: 67.88% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-1 (1-1573) x US-08-430-787A-3 (1-423)  
QY 18 ATGAAGCTTTGAGCCTTGACGCTTCAGTCCCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 77  
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
QY 78 TTCGCGTTCACAGAGTGGCCAAAGTTCTAGCTGCTCTTCCAGAACCTCTTAGGCAAGTTCAA 137  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 138 GTTCTACAGAACTTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 197  
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 198 CTTATTGTGAGAAAAACAAAGTCCATTTTTTGTAAATGCATCTGATGTCGCAATGTG 257  
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
QY 258 AAAGCCCATTTAAATGTGACGCGAAATTCATGCAGTGTCTTGTGGCAGACGCTGGAAGAT 317



Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Qy 318 CTTATTCAACAGCAGATTTCCACGACACAGCTCAGCCCGAGCTCCGCTGCTACTAT 377  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerIleTyr 120  
Qy 378 GAACAGTATCACTCACTAAATCTATTCTTGGATAGATTTATAACTGAGAGCAT 437  
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Qy 438 CCTGATATGCTTACAAAATCCACATTTGGATCTCTATTCAGAAAGTACCCACTATGTT 497  
Db 141 ProAspMetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrVal 160  
Qy 498 TTTAAAGTTTCTGAAAGAACAAACAGCCAAATATGCCATATGATTGCTGGAATC 557  
Db 161 LeuIleValSerGlyIleGlnThrAlaIleAsnAlaIleTrpIleAspCysGlyIle 180  
Qy 558 CATGCCAGAGAATGATCTCTCTGCTTCTGCTTGTGGTTTCATAGGCCAT----- 608  
Db 181 HisAlaArgGlnTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200  
Qy 608 ----- 608  
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220  
Qy 609 -----AATCGAATGTCGAGAAAG 626  
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpIleLysAsnArgMetTrpArgLys 240  
Qy 627 AACCGTTCTTTCTATGCGAACAATCATTTGCATCGGACAGACCTGAATAGCAACTTTGTC 686  
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
Qy 687 TCCAACACTGGTGTGAGGAGGTGCATCCAGTTCTCTCATGCTCGGAAACCTACTGTGGA 746  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280  
Qy 747 CTTTATCTCAGTCAGAACAGAGTGAAGCGAGTGGCTAGTTCTTGTGAGAAGAAATATC 806  
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300  
Qy 807 AACGAGATTAAAGCATACATCAGCATCATTCATCTCCAGCATATAGTGTTCATAT 866  
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320  
Qy 867 TCCTATACAGAGTAAAGCAAGACCATGAGGAAGTCTCTAGTAGGCAAGCA 926  
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340  
Qy 927 GTTCGTGCTATTGACAAAACCTAGTAAAATACCAGGTATACATGCGCCATGCTCAGAA 986  
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360  
Qy 987 ACCTTATACCTAGTCTCTGAGGTGGGACCATTTGATCTATGATTTGGGCATCAATAT 1046  
Db 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspSerTrpIleTyrAspLeuGlyIleLysTyr 380  
Qy 1047 TCGTT-----TAC 1054  
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400  
Qy 1055 ATCAAAACCCCTGTAGAGAGCTTTTGGCGCTGTCTCTAAATAGCTGGCATGTCATT 1114  
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrpHisValIle 420  
Qy 1115 AGGAATGTT 1123  
Db 421 ArgAsnVal 423

RESULT 5

US-08-869-057-2

; Sequence 2, Application US/08869057

; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Negashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Plasma  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 23..401  
; US-08-869-057-2  
  
Alignment Scores:  
Pred. No.: 3,37e-200 Length: 423  
Score: 1885.00 Matches: 365  
Percent Similarity: 86.52% Conservative: 1  
Best Local Similarity: 86.29% Mismatches: 3  
Query Match: 67,88% Indels: 55  
DB: 2 Gaps: 2  
  
US-09-980-881A-1 (1-1573) x US-08-869-057-2 (1-423)  
Qy 18 ATCAAGCTTTGCAGCCTTGCAGCTCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 77  
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Qy 78 TTCGGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTCTAGAACCTCTAGGCAAGTTCAA 137  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Qy 138 GTTCTACAGAACTTTACTACACATATGAGATTGTTCTCTGGCAGCCGCTAACAGCTGAC 197  
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
Qy 198 CTTATTGTCAAGAAAAACAAGTCCATTTTGTAAATGCATCTCATGTCCACAAATGTG 257  
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
Qy 258 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGGCAGACCTGGAAGAT 317  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100

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QY 318 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGCCCGAGCCCTCCGCGCATCGTACTAT 377
Db 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerTyrTyr 120
QY 378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 437
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 438 CCTGATATGCTTCAAAAAATCCACATTGGATCTCATTTGAGAAAGTACCCACTCTATGTT 497
Db 141 ProAspMetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrVal 160
QY 498 TTTAAAGTTTCTGGAAGAAGCAACAGCCAAAATGCCATATGATGGATCTGGNATC 557
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 558 CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGGTTTCATAGGCCAT----- 608
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 608 ----- 608
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 609 -----AATCGAATGTGGAGAAAG 626
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysAsnArgMetTrpArgLys 240
QY 627 AACCGTTCTTCTATGCGAACACATCTTGCATCGAACACAGCTGTAATAGCACTTTGTC 686
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 687 TCACAAACACTGGTGTAGGAGGTGCATCCAGTTCTCATCTGCTCGGAAACCTACTGTGGA 746
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 747 CTTTATCTCAGTCAGACAGACAGAGTGAAGCAGTGGCTAGTTCTTGAGAGAAATATC 806
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 300
QY 807 AACCAGATTAAGCATACATCAGCATGCACTTCACTCCAGCATATAGTGTGTTTCCATAT 866
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 867 TCCTATACACGAAGTAAAGCAACAGACCATGAGGAATGTCTCTAGTAGCCAGTGAAGCA 926
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 927 GTTCGTCTATTGACAAAACCTAGTAAANAATACAGGTATACACATGGCCATGGCTCAGAA 986
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 987 ACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAAAATAT 1046
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1047 TCGTT-----TAC 1054
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1055 ATCAAAACCCAGCTGTAGAGAGCTTTTCCGCTGTCTCTAAATAGCTTGGCATGTCTATT 1114
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrpHisValIle 420
QY 1115 AGGAATGTT 1123
Db 421 ArgAsnVal 423
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## RESULT 6

US-09-813-133A-4

; Sequence 4, Application US/09813133A

; Patent No. 6455294

## ; GENERAL INFORMATION:

```
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
; US-09-813-133A-4
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## Alignment Scores:

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Pred. No.: 5,6e-199 Length: 423
Score: 1874.00 Matches: 363
Percent Similarity: 86.05% Conservative: 1
Best Local Similarity: 85.82% Mismatches: 5
Query Match: 67.48% Indels: 55
DB: 4 Gaps: 2
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US-09-980-881A-1 (1-1573) x US-09-813-133A-4 (1-423)

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QY 18 ATCAAGCTTTGCGACCTTGCAGTCTTGACCTTGACCCATTGTTCTTCTCTGAGCAGCATGTC 77
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 78 TTCGCGTTCCAGAGTGGCCAAAGTTCTAGCTGCTTCTTCTAGAACCTCTTAGCAAGTTCAA 137
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 138 GTTCTACAGAACTTACTACACATATGATGATTGTTCTCTGGCAGCGGTGAACAGCTGAC 197
Db 41 ValLeuGlnAsnLeuThrThrTyrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 198 CTTATTGTGAGAAAACAGTCCATTGTTTGTAAATGCATCTGATGTCGACAAATGTG 257
Db 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
QY 258 AAAGCCCATTTAAATGTGAGCGAAATTCATGCAGTGTCTTGTGGCAGACGTGGAGAT 317
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 318 CTTATTCAACAGCAGATTTCCAAACGACACAGTACAGCCCCGAGCCTCCGATCGTACTAT 377
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerTyrTyr 120
QY 378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 437
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 438 CCTGATATGCTTCAAAAAATCCACATTGGATCTCATTTGAGAAAGTACCCACTCTATGTT 497
Db 141 ProAspMetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrVal 160
QY 498 TTTAAAGTTTCTGGAAGAAGCAACAGCCAAAATGCCATATGATGGATCTGGNATC 557
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 558 CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGGTTTCATAGGCCAT----- 608
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 608 ----- 608
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 609 -----AATCGAATGTGGAGAAAG 626
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
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QY 627 AACCGTTCTTCTATCGGAACAATCATGTGCAACAGACCTGAATAGCAACTTTGTC 686
DB 241 AsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPhaAla 260
QY 687 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCCTCATGCTCGGAACCTACTGTGGA 746
DB 261 SerLysHisTrpCysGluGluAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 747 CTTTATCTGAGTCAGACCAAGACAGTGAAGCAGTGGCTAGTTCTTGGAGNAGAAATATC 806
DB 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 300
QY 807 AACCCAGATTAAAGCATATACATCAGCATGCATTCACTCCACAGCATATAGTGTTCCTAT 866
DB 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 867 TCCTATACAGAACTAAAGCAAGACCATGAGAACTGCTCTAGTAGCCAGTGAAGCA 926
DB 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 927 GTTCGCTCTATTGACAAACTAGTAAATAATACAGGTATACACATGCCCATGGCTCAGAA 986
DB 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 987 ACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAAAATAT 1046
DB 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1047 TCGTT-----TAC 1054
DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1055 ATCAACCCACCTGTAGAGAGCTTTTGGCGCTGTCCTAAATAGCTTGGCATGTCATT 1114
DB 401 IleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrpHisValIle 420
QY 1115 AGGAATGTT 1123
DB 421 ArgAsnVal 423

RESULT 7
US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 415/266-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 417 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-649-591B-7

Alignment Scores:

Pred. No.: 1,14e-63

Score: 655.00

Percent Similarity: 51.67%

Best Local Similarity: 35.89%

Query Match: 23.59%

DB: 1

Length: 417

Matches: 150

Conservative: 66

Mismatches: 138

Indels: 65

Gaps: 9

US-09-980-881A-1 (1-1573) x US-07-649-591B-7 (1-417)

QY 33 CTTGCGAGTCTTGTACCCATTGTTCTTCTGTGAGCAGCATGCTCTCGGTTCCAGAGT 92

DB 7 MetAlaValIleTyrThrThrLeuAlaIleAlaProValHis-----PheAspArg 23

QY 93 GGCAGAGTTCTAGCTGCTCTTCCAGAACCTCTAGCAAGTTCAAGTTCTACAGAACTCTT 152

DB 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43

QY 153 ACTPACACATATGAGATGTTCTCTGCGACCGGTAAACAGCTGACCTTATTGTGAAGAAA 212

DB 44 ThrGlnSerIleGluLeuAspPheTyrTyrProAspAlaIleHisAspIleAlaValAsn 63

QY 213 AAACAAGTCCATTTTGTAAATGATCTGATGTGCACATGTGAAGCCCATTTAAAT 272

DB 64 MetThrValAspPheArgValSerGluLysGlnThrIleGlnSerThrLeuGlu 83

QY 273 GTGAGCGGAATTCATGCGAGTGTCTGCGCAGAGCTGGAAGATCTTATTCAACAGCAG 332

DB 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluIleGluLysGln 103

QY 333 ATTTC-----AACGACACAGTACGCCCGCGAGCTCCGACATCGTACTATGAACATATCAC 389

DB 104 PheAspValLysAspGluIleAlaGlyArgHisSer-----TyrAlaLysTyrAsn 120

QY 390 TCACTAAATGAATCTATTCTTGGATAGAAATTTATACCTGAGAGGATCTCTGATATGCTT 449

DB 121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140

QY 450 ACAAAATCCACATTCGATCCCTCATTTGAGAAAGTACCCACTCTATGTTTAAAGGTTTCT 509

DB 141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159

QY 510 GGAAAAAGAACAAACAGCCAAATGCCATATGGATTGACTGTGGAAATCCATGCCAGAGAA 569

DB 160 GlyLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179

QY 570 TGGATCTCTCTGCTTCTTCTGCTGTGTTCTATA-----GGCCAT 608

DB 180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199

QY 609 AAT----- 611

DB 200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219

QY 612 -----CGAATGTGGAGAAAGAACCGTCTTCTTC 638

DB 220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239

QY 639 TATGCGAACAAATCATTCGATCGAACAGACCTGAATAGCACTTTCTCCCAACACTGG 698

DB 240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258

QY 699 TGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGAAACCTACTGTGAGCTTTTATCTGAG 758



Db 279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298  
Qy 819 GCATACATCAGTCATCATCTCCAGCATATAGTGTTCATATCTTATACAGA 878  
Db 299 AlatyIleThrPheHisSerTyrSerGlnMetLeuLeuProTyrGlyTyrThrPhe 318  
Qy 879 AGTAAACAAAGACCATGAGCACTCTCTAGTACCCAGTGAAGCAGTTCGTGTATT 938  
Db 319 LysLeuProProAsnHisGlnAspLeuLysValAlaArgIleAlaThrAspAlaLeu 338  
Qy 939 GACAAACTAGTAAATACAGTATACATGCGCCATGCTCAGAAACCTTATACCTA 998  
Db 339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357  
Qy 999 GCTCCTGAGGTGGGACGATTGATCTATGATTGGGCATCAAAATATCGTTTAC--- 1054  
Db 358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377  
Qy 1055 -----ATCAAAACCCACC 1066  
Db 378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397  
Qy 1067 TGTAGAGAACTTTGCGGTCTCTCTAAATAGCTTGGCATGTCATTAGGAAT 1120  
Db 398 CysLysGluThrMetLeuSerValLysPheIleAlaLysTyrIleLeuLysAsn 415

RESULT 9

US-08-430-787A-7  
; Sequence 7, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430, 787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELE: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-430-787A-7  
Alignment Scores:  
Pred. No.: 1,14e-63 Length: 417  
Score: 655.00 Matches: 150  
Percent Similarity: 51.67% Conservative: 66  
Best Local Similarity: 23.89% Mismatches: 138  
Query Match: 35.59% Indels: 65  
DB: 1 Gaps: 9  
US-09-980-881A-1 (1-1573) x US-08-430-787A-7 (1-417)  
Qy 33 CTTCAGTCTCTTGTACCCATTTCTCTCTGTGAGCAGCATGCTTTCGGTGTCCAGAGT 92  
Db 7 MetAlaValIleTyrThrLeuAlaIleAlaProValHis-----PheAspArg 23  
Qy 93 GGCCAAAGTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTTCAAGTTCTTACAGAATCTT 152  
Db 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43  
Qy 153 ACTACACATATGATGATTCTTCTGCGCAGCCGTAACAGCTGACCTTATTGTGAAGAAA 212  
Db 44 ThrGlnSerIleGluLeuAspPheTrpTyrProAspAlaIleHisAspIleAlaValAsn 63  
Qy 213 AAACAAGTCCATTTTCTGTAATGATCTGATGTCGACAATGTAAGCCCAATTTAAAT 272  
Db 64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83  
Qy 273 GTGAGCGGAATTCATGCTGCTTCTGTCGAGCAGCTGGAAGATCTTATTCAACAGCAG 332  
Db 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluIleGluLysGln 103  
Qy 333 ATTTC---AAGCAGCAGTACGCCGCCGCTCGCATCGTACTATGAAACAGTATCAC 389  
Db 104 PheAspValLysAspGluIleAlaGlyArgHisSer-----TyrAlaLysTyrAsn 120  
Qy 390 TCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGGCATCTGATATGCTT 449  
Db 121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140  
Qy 450 ACAAAATCCATCTGGATCTCTTGTGAGAGTACCCACTCTATGTTTAAAGGTTTCT 509  
Db 141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159  
Qy 510 GGAAGAAGAACAAACAGCCAAATGCCATATGATGATGATGATGATGATGATGATGATGATGAT 569  
Db 160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179  
Qy 570 TCGATCTCTCTGCTTCTGCTTGTGTTTCATA-----GGCCAT 608  
Db 180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199  
Qy 609 AAT----- 611  
Db 200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219  
Qy 612 -----CGAATGTGGAGAAAGAACCGTCTTTTC 638  
Db 220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239  
Qy 639 TATGCGAACATCATTGATCGGACAGACCCGTGAATAGCACTTCTCTCCAAACACTCG 698  
Db 240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258  
Qy 699 TGTGAGGAAGGTGCATCCAGTCTCTCATGCTCGGAAACCTACTGTGGAATTTTCTCTGAG 758  
Db 259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278  
Qy 759 TCAGAACCAAGAGTGAAGCAGTGGCTGATGTTTCTTGTGAGAGAAATATCAACAGATTAA 818  
Db 279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298

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QY 819 GCATACATCAGCATGCTATCATCTCCAGCATATAGTGTTCATATTCCTATACAGA 878
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
299 AlatyrlleThrPheHisSerTyrSerGlnMetLeuLeuLeuProTyrGlyTyrThrPhe 318
QY 879 AGTAAACCAAGACCATGAGCACTCTCTAGTACCCAGTGAAGCAGTTCGTGCTATT 938
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 LysLeuProProAenHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338
QY 939 GACAAAATAGTAAAAATACAGCATATACATGCGCATGGCTCAGAAACCTTATACCTA 998
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357
QY 999 GCTCCTCGAGTGGGACGATGATCTATGATTTGGGATCAAAATATTCGTTTAC---- 1054
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyIleLysHisThrPheAlaPhe 377
QY 1055 -----ATCAACCCACC 1066
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397
QY 1067 TGATAGAGAAGCTTTTGGCGGTCTCTAAATAGCTTGGCATGTCTATTAGGAAT 1120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
398 CysLysGluThrMetLeuSerValLysPheIleAlaLysTyrIleLeuLysAsn 415

RESULT 10
US-08-860-882A-57:
; Sequence 57, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGLESTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860.882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-882A-57

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Alignment Scores: 2.78e-63 Length: 415
Pred. No.: 651.50 Matches: 142
Score: 52.03% Conservative: 76
Percent Similarity: 33.89% Mismatches: 140
Best Local Similarity: 23.46% Indels: 62
Query Match: 2 Gaps: 8
DB:

US-09-980-881A-1 (1-1573) x US-08-860-882A-57 (1-415)
QY 33 CTTGTCAGTCTCTGTACCCATTGTTCTCTGTGAGCAGCATCTCTTCGGC---TTCCAG 89
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 LeuValValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGluHisPheGlu 21
QY 90 AGTGGCCAGTCTTACGTCGCTCTTCTTAACCTCTAGGCAAGTTCAAGTTCTACAGAAT 149
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
22 GlyGluLysValPheArgValAsnValGluAsnHisIleAsnIleIleArgGlu 41
QY 150 CTTACTACACATATGAGATTGTTCTGTGACCGGTAAACAGCTGACCTTATTGTGAAG 209
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
42 LeuAlaSerThrThrGlnIleAspPheTyrPheProAspSerValThrGlnIleLysPro 61
QY 210 AAAAAACAACTCCATTGTTTAAATGATCTGATGTCGACAAATGTGAAAGCCCATTTA 269
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81
QY 270 AATGTGCGGAATTCATGTCAGTGTCTGTGCGGACAGCTGGAAGATCTTATTCAACAG 329
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 LysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnValAlaGluAla 101
QY 330 CAGATTTCCAAACACACAGCTACGCCCCCGAGCTCCGTCATCTGCTATGACAGTATCAC 389
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
102 GlnPheAspSerArgVal-----A-galathrGlyHisSerTyrGluLysTyrAsn 118
QY 390 TCCTAAATGAAATCTATTCTCGATAGATTTTATACTGAGAGGCATCTCTGATGCTT 449
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 LysTrpGluThrIleGluAlaTrpThrGlnValAlaThrGluAsnProAlaLeuIle 138
QY 450 ACAAATCCACATTTGATGCTCTCATTTGAGAACTACCATCTATGTTTAAAGTTTCT 509
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeuLysVal-- 157
QY 510 GGAAGAACAAACACAGCCAAATGTCATGATGATGCTGGAATCCATGCCAGAGAA 569
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177
QY 570 TGGATCTCTCTGCTTTCTGCTTGTGTTCATA----- 602
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrGlyArg 197
QY 602 ----- 602
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
198 GluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuProValLeuAsn 217
QY 603 -----GGCCAT-----AATCGAATGGAGAAAGACCGTTCTTTC 638
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
218 IleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237
QY 639 TATGCGAAACAATCATTCGTCGGAACAGACCTGAATAGCAACTTTGTCTCCAACATCGG 698
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256
QY 699 TGTGAGGAAGGTGATCCATGCTCTCATGCTCGAAACCTACTGTGCACTTTATCCCTGAG 758
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyProAlaAlaGlu 276
QY 759 TCAGAACCAAGTGAAGGAGTGGCTAGTTCTTGTGAGAAAGAAATATCAACACGATTAAA 818
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 SerGlnLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296
QY 819 GCATACATCAGCATTCATCTACTCCAGCATATAGTGTTCATATTCCTATACAGA 878
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 297 AlaTyrLeuThrIleHisSerTyrSerGlnMetMetIleTyrProTyrSerTyrAlaTyr 316  
Qy 879 AGTAAAGACCAAGACAGTGTCTCTAGTACGAGTGAAGCAGTTCGGCTATT 938  
Db 317 LysLeuGlyGluAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336  
Qy 939 GACAAAACTAGTAAATAACAGGTATACACATGCGCCATCGCTCAGAAACCTTATACCTA 998  
Db 337 --AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrIleTyrPro 355  
Qy 999 GCTCTCGAGTGGGAGGATGATCATGATTTGGCATCAAAATATGCTTTACATC- 1057  
Db 356 AlaAlaGlyGlySerAspThrPalatyrAspGlnGlyIleArgTyrSerPheThrPhe 375  
Qy 1058 -----AAACCCACC 1066  
Db 376 GluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIleArgAlaThr 395  
Qy 1067 TGTAGAGAAGCTTTGCGCTGTCTCTAAATAGCTTGGCATGTCTAGGAATGTT 1123  
Db 396 CysGluGluThrPheLeuAlaIleLysTyrValAlaSerTyrValLeuGluHisLeu 414

## RESULT 11

US-09-011-769A-39  
; Sequence 39, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-011-769A-39  
Alignment Scores:  
Pred. No.: 2.78e-63 Length: 415

Score: 651.50 Matches: 142  
Percent Similarity: 52.03% Conservative: 76  
Best Local Similarity: 33.89% Mismatches: 140  
Query Match: 23.46% Indels: 62  
DB: 4 Gaps: 8  
US-09-980-881A-1 (1-1573) x US-09-011-769A-39 (1-415)  
Qy 33 CTTCGAGTCTCTGTACCCATTTCTCTCTGTGAGCAGCATCTCTTCGCG- ---TTCAG 89  
Db 2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisGlyGlyGluHisPheGlu 21  
Qy 90 AGTGGCAAGTCTAGCTCTCTCTCTAGAACCTCTAGGCAAGTTCAGAGTTCACAGAA 149  
Db 22 GlyGluLysValPheArgValAsnValGluAspGluAsnHisIleAsnIleIleArgGlu 41  
Qy 150 CTTACTACACATATGAGATTGTCTCTGGCAGCCGCTAACAGCTGACCTTATTGTGAAG 209  
Db 42 LeuAlaSerThrThrGlnIleAspPheTrpLysProAspSerValThrGlnIleLysPro 61  
Qy 210 AAAAAACAAGTCCATTTTGTAAATGCATCTGTGTCGACAATGTGAAGCCCATTTA 269  
Db 62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81  
Qy 270 AATGTGAGCGGAATTCATGCTGCTGCTGCGAGAGTGAAGATCTTATTCAACAG 329  
Db 82 LysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101  
Qy 330 CAGATTTCCAAACGACACAGTCAGCCCGGAGCTCCGCATCGTACTATGAAAGTATCAC 389  
Db 102 GlnPheAspSerArgVal-----ArgAlaThrGlyHisSerTyrGluLysTyrAsn 118  
Qy 390 TCACATAATGAATCTATTCTTGATAGAAATTTATACTGAGAGGCTCTGATATGCTT 449  
Db 119 LysTrpGluThrIleGluAlaTrpThrGlnGlnValAlaThrGluAsnProAlaLeuIle 138  
Qy 450 AAAAAATCCATTCGATCTCATTTGAGAGTACCCACTCTATGTTTAAAGTTTCT 509  
Db 139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeuLysVal- 157  
Qy 510 GGAAGAACAACACGCCAAATGCCATATGATGATGCTGCGAATCCATGCCAGAGAA 569  
Db 158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177  
Qy 570 TGGATCTCTCCGCTTTCTGCTGCTGCTCAT- - - - - 602  
Db 178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrGlyArg 197  
Qy 602 ----- 602  
Db 198 GluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuProValLeuAsn 217  
Qy 603 -----GGCAT-----AATCGAATCTGGAGAAAGAACCGTTCTTTC 638  
Db 218 IleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237  
Qy 639 TATGCGAACAAATCATTCGATCGAAGACAGACCTGAATAGCAACTTCTCTCCAAACACTGG 698  
Db 238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256  
Qy 699 TGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGCACTTTTTCCTGAG 758  
Db 257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyProAlaAlaGlu 276  
Qy 759 TCAGAACCAAGTGAAGCAGTGGCTAGTTTCTTGAGAGAAATATCAACCAAGATTAA 818  
Db 277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296  
Qy 819 GCATACATCAGCATGCTCATCTACTCCAGCATATAGTGTTCCTCATTTTCCATATTCATACGA 878  
Db 297 AlaTyrLeuThrIleHisSerTyrSerGlnMetMetIleTyrProTyrSerTyrAlaTyr 316  
Qy 879 AGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTCTATT 938









Qy	1032	TTGGGCATCAAAATATTTCGTTTAC-----	1054
Db	369	LeuGlyIleIysHisThrPheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeu	388
Qy	1055	-----ATCAACCCACCTGTAGAGAGCTTTTGGCGCTGCTCTAAATA	1099
Db	389	LeuProGluSerArgIleLysProThrCysArgGluThrMetLeuAlaValLysPheIle	408
Qy	1100	GCTTGGCATGTCATTAGGAAT	1120
Db	409	AlaLysTyrlleLeuLysHis	415

RESULT 14  
US-08-430-787A-6  
; Sequence 6, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase

Alignment Scores:		
Pred. No.:	7,766-63	417
Score:	647.50	Matches: 143
Percent Similarity:	52.46%	Conservative: 81
Best Local Similarity:	33.49%	Mismatches: 132
Query Match:	23.32%	Indels: 72
DB:	1	Gaps: 10

US-09-980-881A-1 (1-1573) x US-08-430-787A-6 (1-417)

QY	6	ATTGCTGTTGGGATGAAGCTTTGACAGCCCTGCAAGTCTCTGTATGCCATTGTTCTCTCTCTGT	65
Db	5	LeuProValGlyLeuIleAlaThrThrLeuAlaIle---AlaProVal-----	19
QY	66	GAGCAGCATGCTCTTCGCGTTTCCAGAGTGtSCAAAGTTCTAGCTGCTCTCTCCTAGAACCTCT	125
Db	20	-----ArgPheAspArgGluIlyseValPheArgValIlyysProGlnAspGlu	34
QY	126	AGGCAAGTTCAAGTTCTCAGCAATCTTA'TTACAAACATGATGAGTGTCTCTCGCAGCCG	185
Db	35	LysGlnAlaAspIleIleLysAspLeuAlaLysThrAsnGluLeuAspPheTyrIlyrPro	54
QY	186	GTAACAGCTGACCTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGATCTGAT	245
Db	55	GlyAlaThrHisHisValAlaAlaAsnMetMecValAspPheArgValSerGluLysGlu	74
QY	246	GTGCACAATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTGTCTGGCGCA	305
Db	75	SerGlnAlaIleGlnSerAlaLeuAspGlnAsnIlyseMethHisTyrGluIleLeuIleHis	94
QY	306	GAGCTGGAAGATCTTATCAACAGCAGATTTTCC---AACGACACAGTGCACCCCGCAGCC	362
Db	95	AspLeuGlnGluIleGluLysGlnPheAspValIlyysGluAspIleProGlyArgHis	114
QY	363	TCCGCATCGTACTATGAACAGCATCTCACTCAATAAGAAATCTATTCTTGGATAGATTT	422
Db	115	Ser-----TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaIleTrpThrGluLys	131
QY	423	ATAACTGAGAGGCATCCTGATATGCTTACAAAATCCACATTCGATCTCATTTTGAGAAG	482
Db	132	MetMetAspLysTyrProGluMetValSerArgIleLysIleGlySerThrValGluAsp	151
QY	483	TACCCATCTCTATGTTTTAAAGGTTCTCGAAAAAGAACAAACAGCCCAAAATGCCATATGG	542
Db	152	AsnProLeuTyrValLeuLysIle---GlyGluLysAsnGluArgLysAlaIlePhe	170
QY	543	ATTGACTGTGGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTGTGGTTCATA	602
Db	171	MetAspCysGlyIleHisAlaArgGluTrpValSerProAlaPheCysGlnTrpPheVal	190
QY	602	-----	602
Db	191	TyrGlnAlaThrLysThrTyrGlyArgLysIleMetThrLysLeuLeuAspArgMet	210
QY	603	-----GGCAT-----AAT	611
Db	211	AsnPheTyrIleLeuProValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsn	230
QY	612	CGAATGTGAGAAGAACCGTTCTTCTATCGCAACATCATTTGCATCGCAACGACCTG	671
Db	231	ArgMetTrpArgLysAsnArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeu	250
QY	672	AATGAGCAACTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTCTCTCATGCTCG	731
Db	251	AsnArgAsnPhe---AsnAlaSerTyrAsnSerIleProAsnThrAsnAspProCysAla	269
QY	732	GAACCTTACTGTGCAGCTTTATCTCTGAGTCAGAACACCAAGTGAAGGCAGTGGCTAGTTTC	791
Db	270	AspAsnTyrArgGlySerAlaProGluSerGluLysGluThrLysAlaValThrAsnPhe	289
QY	792	TTGAGAAGAATAATCAACAGATTAAGCATACATCAGCATGCAATTCATCTCCACGAT	851
Db	290	IleArgSerHisLeuAsnGluIleLys/altyrIleThrPheHisSerTyrSerGlnMet	309
QY	852	ATAGTGTTCATATTCCTTATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTTA	911
Db	310	LeuLeuPheProTyrGlyTyrThrSerLysLeuProProAsnHisGluAspLeuAlaLys	329
QY	912	GTAGCCAGTGAAGCAGTTCGTGCTATTACAAAACCTAGTAAAAATACCGATATACACAT	971
Db	330	ValAlaLysIleGlyThrAspValLeu---SerThrArgTyrGluThrArgTyrIleTyr	348
QY	972	GGCCATGGCTCAGAAACCTTATACCTA3CTCCTGGAGGTGGGACGATTTGGATCTATGAT	1031
QY			

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Db 349 GlyProIleGluSerThrIleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAsp 368
QY 1032 TTGGGCATCAAAATTCGTTTAC----- 1054
Db 369 LeuGlyIleYshisThrPheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeu 388
QY 1055 -----ATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTCTCTCTAAATA 1099
Db 389 LeuProGluSerArgIleLysProThrCysArgGluThrMetLeuAlaValLysPheIle 408
QY 1100 GCTTGGCATCTATTAGGAAT 1120
Db 409 AlalysTyrIleLeuLysHis 415

RESULT 15
US-09-917-254-66
; Sequence 66, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 66
; LENGTH: 417
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-09-917-254-66

Alignment Scores:
Pred. No.: 7,76e-63 Length: 417
Score: 647.50 Matches: 143
Percent Similarity: 52.46% Conservative: 81
Best Local Similarity: 33.49% Mismatches: 132
Query Match: 23.32% Indels: 72
DB: 4 Gaps: 10

US-09-980-881A-1 (1-1573) x US-09-917-254-66 (1-417)
QY 6 ATTGCTGTTGGATGAAGCTTTCGAGCTTGAGTCCTGTACCCATTTGTTCTCTCTGT 65
Db 5 LeuProValGlyLeuIleAlaThrThrLeuAlaIle---AlaProVal----- 19
QY 66 GAGCAGCATGCTCTCGGTTCCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCT 125
Db 20 -----ArgPheAspArgGluLysValPheArgValLysProGlnAspGlu 34
QY 126 AGGCAAGTTCAAGTCTTACAGAAATCTTACTACACATATGAGATTTGTTCTCGGCAGCCG 185
Db 35 LysGlnAlaAspIleIleLysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrPro 54
QY 186 GTAAACAGCTGACCTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGATCATCTGAT 245
Db 55 GlyAlaThrHisHisValAlaAlaAsnMetMetValAspPheArgValSerGluLysGlu 74
QY 246 GTCGACAAATGTGAAGCCCAATTAAATGTGAGCGGAATCCATGCAAGTGTCTTGTGGCA 305
Db 75 SerGlnAlaIleGlnSerAlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHis 94
QY 306 GAGCTGGAAGATCTTATTCAACAGCAGATTTTC---AACGACACAGTGCAGCCCCGAGCC 362
Db 95 AspLeuGlnGluGluIleGluLysGlnPheAspValLysGluAspIleProGlyArgHis 114
QY 363 TCCGCATCGPACTATGAACAGTATCACTAAATGAAATCTATTCTTGGATGAGATTT 422
Db 115 Ser-----TyrAlaLysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLys 131
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QY 423 ATAACTGAGAGGCATCTCGATATGCTTACAAAATCCACATTTGATCTCTCATTTGAGAAG 482
Db 132 MetMetAspLysTyrProGluMetValSerArgIleLysIleGlySerThrValGluAsp 151
QY 483 TACCCCTCTATGTTTAAAGTTTCTGGAAGAAGAACAAACAGCCAAAATGCCATATGG 542
Db 152 AsnProLeuTyrValLeuLysIle---GlyGluLysAsnGluArgArgLysAlaIlePhe 170
QY 543 ATTGACTGTGGAAATCCATCCAGAGAAATGATCTCTCTGCTTCTGCTTGTGCTGTCATA 602
Db 171 MetAspCysGlyIleHisAlaArgGluTrpValSerProAlaPheCysGlnTrpPheVal 190
QY 602 ----- 602
Db 191 TyrGlnAlaThrLysThrTyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMet 210
QY 603 -----GCCCAT-----AAT 611
Db 211 AsnPheTyrIleLeuProValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsn 230
QY 612 CGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACAAATCATTTGTCATCGAACAGACCTG 671
Db 231 ArgMetTrpArgLysAsnArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeu 250
QY 672 AATAGCAACTTGTCTCTCCAAACACTGCTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 731
Db 251 AsnArgAsnPhe---AsnAlaSerTrpAsnSerIleProAsnThrAsnAspProCysAla 269
QY 732 GAAACCTACTGTGGACTTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTTC 791
Db 270 AspAsnTyrArgGlySerAlaProGluSerGluLysGluThrLysAlaValThrAsnPhe 289
QY 792 TTGAGGAAGAAATATCAACCAAGATTAAGCATACATCAGCATGCATTCATCATCCAGCAT 851
Db 290 IleArgSerHisLeuAsnGluIleLysValTyrIleThrPheHisSerTyrSerGlnMet 309
QY 852 ATAGTGTTCCTCATTTCTTATACAGCAAGTAAAGCAAGACCATCAGGAACCTGTCTCTA 911
Db 310 LeuLeuPheProTyrGlyTyrThrSerLysLeuProProAsnHisGluAspLeuAlaLys 329
QY 912 GTAGCAGTGAAGCAGTTCGTGCTATTGACAAAACCTAGTAAATAACAGGTATACACAT 971
Db 330 ValAlaLysIleGlyThrAspValLeu---SerThrArgTyrGluThrArgTyrIleTyr 348
QY 972 GGCATGGCTCAGAACCTTATACCTAGTCTCTGAGGTGGGACCATGTCATTCATGAT 1031
Db 349 GlyProIleGluSerThrIleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAsp 368
QY 1032 TTGGGCATCAAAATATTCTGTTTAC----- 1054
Db 369 LeuGlyIleLysHisThrPheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeu 388
QY 1055 -----ATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTCTCTCTAAATA 1099
Db 389 LeuProGluSerArgIleLysProThrCysArgGluThrMetLeuAlaValLysPheIle 408
QY 1100 GCTTGGCATCTATTAGGAAT 1120
Db 409 AlaLysTyrIleLeuLysHis 415
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Search completed: October 28, 2004, 19:01:02  
Job time : 64.5 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 28, 2004, 18:56:53 ; Search time 202.5 Seconds  
(without alignments)  
5036.953 Million cell updates/sec

Title: US-09-980-881a-1

Perfect score: 2777

Sequence: 1 agaaattgtgtggatg.....aaaaaaaaaaaaaaaaaa 1573

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 2741442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
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  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

Alignment Scores: 9.61e-186 Length: 386  
Pred. No.: 386

No.	Score	Match	Length	DB	ID	Description
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2	1902.5	68.5	386	14	US-10-212-877-2	Sequence 2, Appli
3	1885	67.9	423	14	US-10-379-836-17	Sequence 17, Appli
4	1874	67.5	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1874	67.5	423	14	US-10-212-877-4	Sequence 4, Appli
6	1861.5	67.0	428	15	US-10-115-479-68	Sequence 68, Appli
7	1861.5	67.0	428	15	US-10-115-479-70	Sequence 70, Appli
8	1796	64.7	423	14	US-10-379-836-2	Sequence 2, Appli
9	1592.5	57.3	422	14	US-10-379-836-18	Sequence 18, Appli
10	1568.5	56.5	422	14	US-10-379-836-16	Sequence 16, Appli
11	1492.5	53.7	322	15	US-10-115-479-64	Sequence 64, Appli
12	1446.5	52.1	354	15	US-10-115-479-66	Sequence 66, Appli
13	889	32.0	211	9	US-09-925-302-467	Sequence 467, App
14	889	32.0	211	10	US-09-925-302-467	Sequence 467, App
15	652.5	23.5	417	15	US-10-074-978A-267	Sequence 267, App
16	652.5	23.5	417	15	US-10-074-978A-268	Sequence 268, App
17	652.5	23.5	417	16	US-10-477-515-3	Sequence 3, Appli
18	647.5	23.3	417	14	US-10-229-546-2	Sequence 2, Appli
19	647.5	23.3	417	14	US-10-229-546-9	Sequence 9, Appli
20	647.5	23.3	417	14	US-10-341-434-188	Sequence 188, App
21	647.5	23.3	417	15	US-10-262-511-72	Sequence 72, Appli
22	646	23.3	416	15	US-10-074-978A-269	Sequence 269, App
23	644	23.2	402	14	US-10-379-836-20	Sequence 20, Appli
24	640.5	23.1	416	15	US-10-074-978A-270	Sequence 270, App
25	635.5	22.9	437	13	US-10-200-344-10	Sequence 10, Appli
26	635.5	22.9	437	14	US-10-274-639-12	Sequence 12, Appli
27	635.5	22.9	437	15	US-10-333-574-12	Sequence 12, Appli
28	634.5	22.8	716	9	US-09-910-059-125	Sequence 125, App
29	634	22.8	416	15	US-10-074-978A-266	Sequence 266, App
30	633.5	22.8	437	17	US-10-757-262-128	Sequence 128, App
31	630.5	22.7	434	16	US-10-477-515-2	Sequence 2, Appli
32	571.5	20.6	613	9	US-09-910-059-113	Sequence 113, App
33	571.5	20.6	613	16	US-10-608-710-4	Sequence 4, Appli
34	570	20.5	374	9	US-09-888-615-61	Sequence 61, Appli
35	563	20.3	444	14	US-10-176-306-74	Sequence 74, Appli
36	546.5	19.7	399	14	US-10-200-910-8	Sequence 8, Appli
37	546.5	19.7	399	17	US-10-843-130-8	Sequence 8, Appli
38	536.5	19.3	286	16	US-10-408-765A-1959	Sequence 1959, Ap
39	536	19.3	419	15	US-10-072-012-788	Sequence 788, App
40	529.5	19.1	350	13	US-10-200-344-12	Sequence 12, Appli
41	522	18.8	286	15	US-10-072-012-887	Sequence 887, App
42	520	18.7	419	15	US-10-257-174-40	Sequence 40, Appli
43	520	18.7	436	14	US-10-200-910-6	Sequence 6, Appli
44	520	18.7	436	15	US-10-072-012-784	Sequence 784, App
45	520	18.7	436	15	US-10-257-174-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813, 133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Human

US-09-813-133A-2



Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Qy 438 CCTGATATGCTTCAAAAATCCCATTTGGATCCCTATTTCAGAGAGTACCCACTCTATGTT 497  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrVal 160  
Qy 498 TTAAGGTTTCTGAAAGAACAAACAGCCAAAATGCCATATGATGATTCGTGGAAATC 557  
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Qy 558 CATGCCAGAGATGATCTCTCCCTGCTTCTGCTTGGTTCATAGGCCATATATCGAATG 617  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Qy 618 TGGAGAAAGAACCTGCTTCTATGCGAACAATCATTCGATCGGAACAGACCTGAATAGC 677  
Db 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220  
Qy 678 AACTTTGCTCTCAAACTGCTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAAACC 737  
Db 221 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
Qy 738 TACTGTGCATTTATCTGAGTCAGAACCAAGAGTGAAGCAGGTGGCTAGTTCTTGAGA 797  
Db 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Qy 798 AGAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 857  
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Qy 858 TTTCATATTTCTTATACACGAAGTAAAGCAAGACCATCAGGAACTGTCTCTAGTAGCC 917  
Db 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
Qy 918 AGTGAACAGTTCTGCTATTGACAAAATAGTAAAAATACCAGGTATACACATGGCCAT 977  
Db 301 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 320  
Qy 978 GGCTCAGAACTTATACCTAGCTCCTGGAGGTGGGACCATGGATCTATGATTTGGGC 1037  
Db 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 340  
Qy 1038 ATCAAAATATTCTGTT----- 1051  
Db 341 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 360  
Qy 1052 -----TACATCAAAACCCACTGTAGAGAGCTTTTCCCGCTGTCTCTAAATAGCTGG 1105  
Db 361 GluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrp 380  
Qy 1106 CATGTCATTAGGAATGTT 1123  
Db 381 HisValIleArgAsnVal 386

RESULT 3  
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; Sequence 17, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; TITLE OF INVENTION: TAPI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-379-836-17  
Alignment Scores:  
Pred. No.: 6,17e-184 Length: 423  
Score: 1885.00 Matches: 365  
Percent Similarity: 86.52% Conservative: 1  
Best Local Similarity: 86.29% Mismatches: 3  
Query Match: 67.88% Indels: 55  
DB: 14 Gaps: 2

US-09-980-881A-1 (1-1573) x US-10-379-836-17 (1-423)

Qy 18 ATCAAGCTTTGACGCTTGCAGTCTTGCAGTCTTGTACCCATTGTTCTCTCTGTGACGACGATGTC 77  
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Qy 78 TTGCGCTTCCAGAGTGGCCAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 137  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Qy 138 GTTCTACAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGAC 197  
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
Qy 198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCATCTCATGTGCAAAATGTG 257  
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
Qy 258 AAGCCCTTTAAATGTGACGGAATTCATGCAAGTGTCTTGTGCGACAGCTGGAAGAT 317  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Qy 318 CTTATTTCACAGCAGATTTCCACACAGACAGTCCAGCCCGCCGCGCTCCGCACTGTAAT 377  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Qy 378 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGCAT 437  
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Qy 438 CTGTATATGCTTACAAAATCCACATTTGGATCTCTCATTTTGGAGAGTACCCACTCTATGTT 497  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Qy 498 TTAAGGTTTCTGGAAGAACAAACAGCAACCAAAATGCCATATGCAATCTGCTGGAATC 557  
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Qy 558 CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAT----- 608  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200  
Qy 608 ----- 608  
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220  
Qy 609 -----AATCGAATGTGAGAAAG 626  
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240  
Qy 627 AACCGTTCTTTCTATCGGAACAATCAATTCATCGCAACAGACCTGAATAGCAACTTTGTC 686  
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
Qy 687 TCAAAACACTGTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCGGAAACCTTACTGTGGA 746  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280  
Qy 747 CTTTATCTCTGAGTACAGAACAGAGTGAAGGAGTGGCTAGTTCTTGTGAGAACAAATATC 806  
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300  
Qy 807 AACGAGATTAAAGCATACATCAGCATGTCATTCTACTCCAGCATATAGTGTTCATAT 866

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Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
Qy 867 TCCTATACAGAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 926
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
Qy 927 GTTCGTGCTATTGACAAACTAGTAAATAACAGGTATACACATGGCCATGGCTCAGAA 986
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
Qy 987 ACCTTATACCTAGCTCCTGGAGGCGGACGATTGGATCTATGATTTGGGCATCAAAATAT 1046
Db 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspSerPheIleTyrAspLeuGlyIleLysTyr 380
Qy 1047 TCGTT-----TAC 1054
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
Qy 1055 ATCAAAACCCTGTAGAGAGCTTTTGGCGCTGTCTCTAAATAGCTTGGCATGTCAAT 1114
Db 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLysIleAlaTrpHisValIle 420
Qy 1115 AGGAATGTT 1123
Db 421 ArgAsnVal 423

RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CU001173
; CURRENT APPLICATION NUMBER: US/09/813.133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Alignment Scores:
Pred. No.: 8.28e-183 Length: 423
Score: 1874.00 Matches: 363
Percent Similarity: 86.05% Conservative: 1
Best Local Similarity: 85.82% Mismatches: 5
Query Match: 67.48% Indels: 55
DB: 9 Gaps: 2

US-09-980-881a-1 (1-1573) x US-09-813-133A-4 (1-423)
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Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Qy 78 TTCGGTTCAGAGTGGCAAGTCTAGCTCTTCTTAGAACCTCTAGCAAGTTCAA 137
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
Qy 138 GTTCTACAGATCTTACTACAAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 197
Db 41 ValLeuGlnAsnLeuThrThrTyrGlyIleValLeuTrpGlnProValThrAlaAsp 60
Qy 198 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG 257
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
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Qy 258 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTGCTGCGACAGCGTGAAGAT 317
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Qy 318 CTTATTCAACAGCAGAGATTTCCAAACGACACAGTCAGCCCGCCGAGCCCTCCGATCGTACTAT 377
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Qy 378 GAACAGTATCCTACCTAAATGAATCTATTCTTGGATAGAAATTTATACTAGAGAGCAT 437
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Qy 438 CCTGATATGCTTACAAAATCCACATTCATCTCATTTGAGAGTACCCACTCTATGTT 497
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Qy 498 TTAAGGTTTCTCGAAAGAACAAACAGCCAAAATGCCATATGGATTTGACTGTGGAATC 557
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Qy 558 CATGCCAGAGAATGGATCTCTCTGCTTCTGCTTGTGGTTTCATAGGCCAT----- 608
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
Qy 608 ----- 608
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
Qy 609 -----AATCGAATGTGAGAAAG 626
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
Qy 627 AACCGTTCTTCTATCGGAACAATCTTCATCGGAACAGACCTGAATAGCACTTTGTC 686
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Qy 687 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGTCGGAACACTACTGTGA 746
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerSerSerSerSerSerSer 280
Qy 747 CTTTATCCTGAGTCAGAACCCAGAAAGTGAGGCGAGTGGCTAGTTTCTTGAGAAAGAAATATC 806
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
Qy 807 AACGAGTTAAAGCATATCATCAGCATGCNTTCTACTCCAGCATATAGTGTTCATAT 866
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
Qy 867 TCCTATACAGAAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 926
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Qy 927 GTTCGTGCTATTGACAAACTAGTAAATAACAGGTATACACATGGCCATGGCTCAGAA 986
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Qy 987 ACCTTATACCTAGCTCCTGGAGTGGGACGATTCATCTATGATTTGGGCATCAAAATAT 1046
Db 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyr 380
Qy 1047 TCGTT-----TAC 1054
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
Qy 1055 ATCAAAACCCTGTAGAGAGCTTTTGGCGCTGTCTCTAAATAGCTTGGCATGTCAAT 1114
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Qy 1115 AGGAATGTT 1123
Db 421 ArgAsnVal 423

RESULT 5
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; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stracie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

Alignment Scores:
Pred. No.: 1,59e-181 Length: 428
Score: 1861.50 Matches: 363
Percent Similarity: 85.05% Conservative: 1
Best Local Similarity: 84.81% Mismatches: 5
Query Match: 67.03% Indels: 60
DB: 15 Gaps: 3

US-09-980-881A-1 (1-1573) x US-10-115-479-70 (1-428)

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Qy 78 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 137
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProargThrserArgGlnValGln 40
Qy 138 GTTCTTACAGAACTTACTTACAACATATGAGATGTTCTTCTGGCAGCGGTAACAGCTGAC 197

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Qy	867	TCCTATACAGAAAGCAACCAAGCACTGTCTCTAGTAGCCAGTGACCA	926
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Qy	927	GTTCGTGCTATTGCACAAACCTAGTAAATAATACCAGGTATACACATGGCCATGGCTCAGAA	986
Dy	927		
Db	340	ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu	359
Qy	987	ACCTTATACCTAGCTCTCGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAAAATAT	1046
Dy	987		
Db	360	SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleLysTyr	379
Qy	1047	TCGTT-----TAC	1054
Dy	1047		
Db	380	SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgTyr	399
Qy	1055	ATCAAAACCCACCTGTAGAGAGCTTTTGGCGCTCTCTAAATAGCTTGGCATGTCAAT	1114
Dy	1055		
Db	400	IleLysProThrCysAlaGluAlaLeuAlaAlaIleSerLysIleValTrpHisValIle	419
Qy	1115	AGGAAT 1120	
Dy	1115		
Db	420	ArgAsn 421	
RESULT 10			
US-10-379-836-16			
; Sequence 16, Application US/10379836			
; Publication No. US20030215850A1			
; GENERAL INFORMATION:			
; APPLICANT: Bristol-Myers Squibb Company			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON			
; TITLE OF INVENTION: TAFI			
; FILE REFERENCE: D0214NP			
; CURRENT APPLICATION NUMBER: US/10/379,836			
; CURRENT FILING DATE: 2003-03-04			
; PRIOR APPLICATION NUMBER: U.S. 60/361,523			
; PRIOR FILING DATE: 2002-03-04			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 16			
; LENGTH: 422			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
US-10-379-836-16			
Alignment Scores:			
Pred. No.:	1.76e-151	Length:	422
Score:	1568.50	Matches:	305
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Best Local Similarity:	72.27%	Mismatches:	36
Query Match:	56.48%	Indels:	56
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US-09-980-881A-1 (1-1573) x US-10-379-836-16 (1-422)			
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Dy	18		
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Qy	78	TTGCGTTTCAGAGTGGCCAGTTCTAGCTGCTTCTTAGAACCTCTAGGCAAGTTCAA	137
Dy	78		
Db	20	LeuAlaPheGlnSerGlyHisValLeuSerAlaLeuProArgThrSerArgGlnValGln	39
Qy	138	GTTCCTACAGATCTTACTACAACATAGATGTTCTCTGGCAGCCGGTAACAGCTGAC	197
Dy	138		
Db	40	LeuLeuGlnAsnLeuThrThrTyrGluValValLeuTrpGlnProValThrAlaGlu	59
Qy	198	CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAATGTG	257
Dy	198		
Db	60	PheIleGluLysLysLysGluValHisPhePheValAsnAlaSerAspValAsnSerVal	79
Qy	258	AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTCTCTTGTGCGAGACGTGGAGAT	317
Dy	258		

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Db      80  LysAlaTyrLeuAsnAlaSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99
Qy      318 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGCCCCGAGCCTCCGATCGTACTAT 377
      |||||
Db      100 LeuIleGlnGlnThrSerAsnAspThrValSerProArgAlaSerSerTyrTyr 119
      |||||
Qy      378 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTTATTAACGTGAGAGCAT 437
      |||||
Db      120 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluValIleThrGluGlnHis 139
      |||||
Qy      438 CCTGATATGCTTACAAAAATCCACATTTGAGTCCTCATTTGAGAAGTACCCACTCTATGTT 497
      |||||
Db      140 ProAspMetLeuGlnLysIleTyrIleGlySerSerTyrGluLysTyrProLeuTyrVal 159
      |||||
Qy      498 TTAAGGTTTCTGGAAGAACAAACAGCCCAAAATGCCATATGATGATGAGTGTGGAATC 557
      |||||
Db      160 LeuLysValSerGlyLysGluHisArgValLysAsnAlaIleTyrIleAspCysGlyIle 179
      |||||
Qy      558 CATGCCAGAGATGATCTCTCCTGCTTCTGCTTGGTGGTTCATAGGCCAT----- 608
      |||||
Db      180 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyTyrValThrGln 199
      |||||
Qy      608 ----- 608
Db      200 PheHisGlyLysGluAsnThrTyrThrArgLeuLeuArgHisValAspPheTyrIleMet 219
      |||||
Qy      609 -----AATCGAATGTGGAGAAAG 626
      |||||
Db      220 ProValMetAsnValAspGlyTyrAspTyrThrTrpLysLysAsnArgMetTrpArgLys 239
      |||||
Qy      627 AACCGTTCTTCTATCGCAACAACTATGTCATCGCAACAGACCTGATAGCACTTTGTC 686
      |||||
Db      240 AsnArgSerValHisMetAsnAsnArgCysValGlyThrAspLeuAsnArgAsnPheAla 259
      |||||
Qy      687 TCCAAACACTGGTGTGAGAAAGTGCACTCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746
      |||||
Db      260 SerLysHisTrpCysGluLysGlyAlaSerSerPheSerCysSerGluThrTyrCysGly 279
      |||||
Qy      747 CTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTGTGAGAGAAATATC 806
      |||||
Db      280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgAsnIle 299
      |||||
Qy      807 AACCAGATTAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTCTTTCCATAT 866
      |||||
Db      300 AsnHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnGlnIleLeuPheProTyr 319
      |||||
Qy      867 TCCTATACACGAAGTAAAGCAAGACCATCAGGAACCTGTCTCTAGTAGCCAGTGAAGCA 926
      |||||
Db      320 SerTyrAsnArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 339
      |||||
Qy      927 GTTCGTGCTATTGACAAACTAGTAAATAACAGGTATACATATGGCCATGGCTCAGAA 986
      |||||
Db      340 ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359
      |||||
Qy      987 ACCTTATACCTAGCTCTGAGAGTGGGACCATTTGATGATTTGGGCATCAAAATAT 1046
      |||||
Db      360 SerLeuTyrLeuAlaProGlyLysSerAspAspTrpIleTyrAspLeuGlyIleLysTyr 379
      |||||
Qy      1047 TCGTTTACATC----- 1057
      |||||
Db      380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgPhe 399
      |||||
Qy      1058 ---AAACCCACTGTAGAGAGCTTTTCCGCTGTCTCTCTAAATAGCTTGCATGTCAATT 1114
      |||||
Db      400 IleLysProThrCysAlaGluAlaLeuAlaValSerLysIleAlaTrpHisValIle 419
      |||||
Qy      1115 AGGAAT 1120
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Db      420 ArgAsn 421
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RESULT 11

US-10-115-479-64

; Sequence 64, Application US/10115479

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; Publication No. US200400006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malvanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 P't)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Alignment Scores:
Pred. No.: 1e-143 Length: 322
Score: 1492.50 Matches: 301
Percent Similarity: 78.24% Conservative: 1
Best Local Similarity: 77.98% Mismatches: 3
Query Match: 53.75% Indels: 82
DB: 15 Gaps: 2

US-09-980-881A-1 (1-1573) x US-10-115-479-64 (1-322)

Qy      18 ATGAAGCTTTGCAGCCTTGAGTCCTTATCCCATTTCTTCTCTGTGAGCAGCATGTC 77
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Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Qy 78 TTCGGTTCCAGAGTCCAGGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 137  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Qy 138 GTTCTACAGAACTTACTACAACATATGAGATTGTTCTTGGCAGCGCGTAAACAGCTGAC 197  
Db 41 ValLeuGlnAenLeuThrThrTyrGluIleValLeuThrGlnProValThrAlaAsp 60  
Qy 198 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTGTAAATGATCTGATGTCGCAATGTG 257  
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
Qy 258 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTCTTGTCTGGCAGAGCGTGAAGAT 317  
Db 81 LysAlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Qy 318 CTTATTCAACAGCAGATTTTCAACGACACACATGTCAGCCCGAGCCTCCGCATCGTACTAT 377  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Qy 378 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATTAACGTGAGGCAT 437  
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Qy 438 CCTGATATGTTCAAAAATCCCATTTGATGCTCTCTTTCAGAGTACCCACTCTATGTT 497  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Qy 498 TTTAAGTTTCTGGAAAGAACCAACCAAGCCAAAATGCCATATGATGATTGACTGTGGAATC 557  
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAsp----- 177  
Qy 558 CATGCCAGAGATGGATCTCTCTGCTTCTGCTTCTGCTTGCATAGGCCATAATCGAATG 617  
Db 177 ----- 177  
Qy 618 TGGAGAAGAACCCTTCTTCTATGCGAACATCATTTGCATCGGAACAGACCTGAATAGC 677  
Db 177 ----- 177  
Qy 678 AACTTTGCTCCAACACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGCTCGGAACCC 737  
Db 177 ----- 177  
Qy 738 TACTGTGGACTTTATCTAGTCAAGAACCGAAGTGAAGCGAGTGGTCTAGTTCTTGAGA 797  
Db 178 ---CysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 196  
Qy 798 AGAATATCAACAGATTAAAGCATATCATGATGATTCATCTACTCCAGCATATAGTG 857  
Db 197 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 216  
Qy 858 TTTCCATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCC 917  
Db 217 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 236  
Qy 918 AGTGAACAGTTCGTCTATTGACAAAACCTAGTAAATAACAGGTATACACATGGCCAT 977  
Db 237 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis 256  
Qy 978 GGCTCAGAAACCTTATACCTAGCTCCCTGGAGTGGGACCATTTGATCTATGTTGGGC 1037  
Db 257 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 276  
Qy 1038 ATCAAAATATTCGTT----- 1051  
Db 277 IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro 296  
Qy 1052 -----TACATCAAAACCCACTGTAGAGAGCTTTTCCCGCTGTCTCTAAATAGCTTGG 1105  
Db 297 GluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLysIleAlaTrp 316

Qy 1106 CATGTCATTAGGAATGTT 1123  
Db 317 HisValIleArgAsnVal 322  
RESULT 12  
US-10-115-479-66  
; Sequence 66, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 66  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-66  
Alignment Scores: 5.39e-139 Length: 354  
Pred. No.: 1446.50 Matches: 291  
Score: 67.99% Conservative: 0  
Percent Similarity: 0



Best Local Similarity: 67.99%		Mismatches: 4	
Query Match: 52.09%		Indels: 134	
DB: 15		Gaps: 4	
US-09-980-881A-1 (1-1573) x US-10-115-479-66 (1-354)			
QY	18	ATGAGCTTTGAGCCTTGAGCTTCTGACCTTCTACCCATTTCTCTCTGAGCAGCATGTC	77
DB	1	MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal	20
QY	78	TTCCGCTTCCAGAGTGCAGGCTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA	137
DB	21	PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln	40
QY	138	GTTCACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC	197
DB	41	ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp	60
QY	198	CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG	257
DB	61	LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal	80
QY	258	AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGCTTCTGGCAGACGTGGAAGAT	317
DB	81	LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp	100
QY	318	CTTATTCAACAGCAGATTTTCAACGACACAGTACGCCCCGAGCCTCCGCATCGTACTAT	377
DB	101	LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr	120
QY	378	GAAACAGTATCACTCACTAAATGAATCTATTCTTGATAGAATTTATAACTGAGAGCAT	437
DB	121	GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis	140
QY	438	CCTGATATGCTTACAAAAATCCATTTGATGATCCTCATTTTGAGAGATGCCCACTCTATGTT	497
DB	141	ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal	160
QY	498	TTAAAG-----GTTTCTGGAAGAAACAAACAGCCCAAAATGCCATATGG	542
DB	161	LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp	180
QY	543	ATTGACTGTGGAATCCATGCCAGAGATGATCTCTCTGCTTTCTGCTTGTGTTGTCATA	602
DB	181	IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	200
QY	603	GGCCAT-----	608
DB	201	GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuVal	220
QY	609	-----AAT	611
DB	221	AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsn	240
QY	612	CGAATGTGAGAAAGACCGTTCTTCTATGCGAACAATCATTCGATCGGAACAGACTG	671
DB	241	ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu	260
QY	672	AATAGCAACTTGTCTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCCTCATGCTCG	731
DB	261	AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer	280
QY	732	GAACACCTACTGTGGACTTTATCTCTGAGTTCAGAACCCAGAAAGTGAAGCGAGTGTTC	791
DB	281	GluThrTyrCysGlyLeuTyrProGlu-----	289
QY	792	TTGAGAGAAATATCAACAGATTAAGCATACATCAGCATGCTTCTACTCCAGCAT	851
DB	289	-----	289
QY	852	ATAGTGTTCATATTCTTATACGAAGTAAAGCAAGCAACCATGAGGAACCTGTCTCTA	911
DB	289	-----	289



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Qy 846 CAGCATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACGTG 905
Db 102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121
Qy 906 TCCTAGTACGAGTGAAGCAGTTCGTCTATTACACAAACTAGTAAATAATACAGGTAT 965
Db 122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyr 141
Qy 966 ACACATGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGAGTGGGACGAGTTGGATC 1025
Db 142 ThrHisGlyHisGlySerGluThrLeuThrLeuAlaProGlyGlyGlyAspAspTrpIle 161
Qy 1026 TATGATTGGGCATCAAAATATTTCGTT----- 1051
Db 162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGly 181
Qy 1052 -----TACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCT 1093
Db 182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSer 201
Qy 1094 AAAATAGCTTGGCATGTCATTAGGAATGTT 1123
Db 202 LysIleAlaIleHisValIleArgAsnVal 211

RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.: 6,74e-82 Length: 211
Score: 889.00 Matches: 173
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 82.38% Mismatches: 9
Query Match: 32.01% Indels: 27
DB: 10 Gaps: 3

US-09-980-881A-1 (1-1573) x US-09-925-302-467 (1-211)
Qy 570 TGGATCTCTCTGTTCTCTGTTGTTGTTTCATAT-----GGC 605
Db 3 TrpIleSer---MetLeuCysArgTrpLeuMetMetValMetAsnTyrSerTrpLys 21
Qy 606 CATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAAATCATTCGATCGGAACA 665
Db 22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThr 41
Qy 666 GACTGTAATAGCAACTTTGTTCTCAAAACATCTGTGTGAGAAAGGTGATCCAGTTCCTCA 725
Db 42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSer 61
Qy 726 TGCTCGAAACCTACTGTCGACTTTATCTCCAGTGCAGAACAGAGTGAAGCGAGTGGCT 785
Db 62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVallyAlaValAla 81
Qy 786 AGTTTCTTGAGAGAAATATCAACCCAGATTAAAGCATATACATGATGATTCATCTCC 845
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Db 82 SerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSer 101
Qy 846 CAGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACGTG 905
Db 102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121
Qy 906 TCCTAGTACGAGTGAAGCAGTTCGTCTATTACACAAACTAGTAAATAATACAGGTAT 965
Db 122 SerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyr 141
Qy 966 ACACATGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGAGTGGGACGAGTTGGATC 1025
Db 142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161
Qy 1026 TATGATTGGGCATCAAAATATTTCGTT----- 1051
Db 162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGly 181
Qy 1052 -----TACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCT 1093
Db 182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSer 201
Qy 1094 AAAATAGCTTGGCATGTCATTAGGAATGTT 1123
Db 202 LysIleAlaIleHisValIleArgAsnVal 211

RESULT 15
US-10-074-978A-267
; Sequence 267, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Hayes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
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; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 267
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-267

Alignment Scores:
Pred. No.: 1.5e-57 Length: 417
Score: 652.50 Matches: 142
Percent Similarity: 52.13% Conservative: 78
Best Local Similarity: 33.65% Mismatches: 141
Query Match: 23.50% Indels: 62
DB: 15 Gaps: 8

US-09-980-881A-1 (1-1573) x US-10-074-978A-267 (1-417)
QY 24 CTTTGACGCTTGAGTCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTTCTCGCG 83
Db 1 MetLeuAlaLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGlu 20
QY 84 ---TTCAGAGTGCCCAAGTTCTAGCTGCTTCTTCTAGAACCTCTAGGCAAGTTCAAGTT 140
Db 21 HisPheGluGlyGlyValPheArgValAsnValGluAspGluAsnHisAlaAsnVal 40
QY 141 CTACAGAACTTCTACTACACATATGAGATGTTCTCTGCGAGCCGGTAACAGCTGACCTT 200
Db 41 IleArgGluLeuAlaSerThrThrGlnIleAspPheThrPheProAspSerValThrGln 60
QY 201 ATTGTGAAGAAAAACAAAGTCCATTGTTTGTAAATGCATCTGATGTCGACAAATGTGAAA 260
Db 61 IleIysProHisSerThrValAspPheArgValLysAlaGluAspThrValThrValGlu 80
QY 261 GCCATTAAATGTGAGCGGAATCCATGAGTGCTGCTGCGAGACGTTGGAAGATCTT 320
Db 81 AsnValLeuLysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnVal 100
QY 321 ATTCAACAGCAGATTTCACAGACACAGTCAGCCCCCGAGCTCCGTCATCGTACTATGAA 380
Db 101 ValGluAlaGlnPheAspSerArgVal-----ArgAlaThrGlyHisSerTyrGlu 117
QY 381 CAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATTAAGTACGAGGCAATCCT 440
Db 118 LysTyrAsnLysTyrGluThrIleGluAlaThrPheGlnValAlaThrGluAsnPro 137
QY 441 GATATGCTTCAAAAATCCACATTTGGATTCCTATTGAGAAGTACCCACTCTATGTTTA 500
Db 138 AlaLeuIleSerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeu 157
QY 501 AAGTTTCTGGAAGAAACAAACAGCCAAATATGCTATGATGATGCTGGAAATCCAT 560
Db 158 LysVal---GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHis 176
QY 561 GCCAGAGAATGGATCTCTCTGCTTTCTGCTGTGGTTCATA----- 602
Db 177 AlaArgGluThrPheSerProAlaPheCysGlnThrPheValArgGluAlaValArgThr 196
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QY 602 ----- 602
Db 197 TyrGlyArgGluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuPro 216
QY 603 -----GCCCAT-----AATCGAATGTGGAGAAAGAAC 629
Db 217 ValLeuAsnIleAspGlyTyrIleTyrThrTyrLysSerArgPheTyrPheGlyThr 236
QY 630 CGTTCTTTCTATCGGAACAATCATTCATCGGAACAGACCTGAATAGCAACTTTGTCTCC 689
Db 237 ArgSerThrHisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---Asp 255
QY 690 AAACACTGTTGTCAGGAAGTGCATCCAGTTCCTCATCTCGCGAAACCTACTCTGGACTT 749
Db 256 AlaGlyTyrCysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyPro 275
QY 750 TATCCTGAGTCAGAACCAAGTGAAGGAGTGGTAGTTCTTGTGAGAAGAAATATCAAC 809
Db 276 AlaAlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSer 295
QY 810 CAGATTAAAGCATATCATCAGCATGCAATTCATCTCCAGCATATAGTGTTCCTATATTC 869
Db 296 SerIleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetIleTyrProTyrSer 315
QY 870 TATACACGAGTAACCAAGACCATGAGGAACCTGCTCTACTAGCAGTGAAGCAGTT 929
Db 316 TyrAlaTyrLysLeuGlyGluAsnAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrVal 335
QY 930 CGTGCTATTGACACAAACTAGTAAAAATACACAGGTATACACATGCCATGGCTCAGAAACC 989
Db 336 LysGluLeu---AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrThr 354
QY 990 TTATACCTAGCTCCTGAGGTGGGACGATTGGATCTATGATTTGGGCATCAATATTCG 1049
Db 355 IleTyrProAlaAlaGlyGlySerAspSerTrpAlaTyrAspGlnGlyIleArgTyrSer 374
QY 1050 TTTTACATC----- 1057
Db 375 PheThrPheGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIle 394
QY 1058 AAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTCTAAATAGCTTGGCATGTATTAGG 1117
Db 395 ArgAlaThrCysGluGluThrPheLeuAlaIleLysTyrValAlaSerTyrValLeuGlu 414
QY 1118 AATGTT 1123
Db 415 HisLeu 416
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Search completed: October 28, 2004, 19:28:11

Job time : 226.5 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 22:52:22 ; Search time 151 Seconds  
(without alignments)  
7404.443 Million cell updates/sec

Title: US-09-980-881A-1  
Perfect score: 1573  
Sequence: 1 agaaattgtctgtgggatg.....aaaaaaaaaaaaaaaaaaaa 1573

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1469.8	93.4	1625	4	US-09-813-133A-1
2	1372	87.2	1749	1	US-07-649-591B-2
3	1372	87.2	1749	1	US-08-277-540-2
4	1372	87.2	1749	1	US-08-430-787A-2
5	918	58.4	1272	2	US-08-869-057-1
6	478.6	30.4	55827	4	US-09-813-133A-3
7	124	7.9	927	5	PCT-US96-00995-5
8	124	7.9	927	5	PCT-US96-00995-5
9	123.4	7.8	921	1	US-08-696-139-3
10	123.4	7.8	1215	1	US-08-696-139-1
11	109	6.9	1263	4	US-09-011-769A-38
12	107.6	6.8	1622	4	US-09-023-655-1020
13	107.4	6.8	999	2	US-08-860-882A-67
14	107.4	6.8	1053	2	US-09-011-769A-50
15	107.4	6.8	1053	2	US-08-860-882A-64
16	107.4	6.8	1053	4	US-09-011-769A-46
17	107.4	6.8	1263	2	US-08-860-882A-56
18	107.4	6.8	1284	2	US-08-860-882A-71
19	107.4	6.8	1284	4	US-09-011-769A-55
20	104.2	6.6	1053	4	US-09-463-451-27
21	104.2	6.6	1053	4	US-09-463-451-28
22	104.2	6.6	1053	2	US-08-860-882A-74
23	104.2	6.6	1053	2	US-08-860-882A-77
24	104.2	6.6	1059	4	US-09-011-769A-59
25	104.2	6.6	1059	4	US-09-011-769A-63
26	101	6.4	1870	3	US-09-171-945-112
27	101	6.4	2154	3	US-09-171-945-124

c

ALIGNMENTS

RESULT 1

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294

; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinhu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; TYPE: DNA

; LENGTH: 1625

; ORGANISM: Human

; US-09-813-133A-1

Query Match	93.4%;	Score 1469.8;	DB 4;	Length 1625;
Best Local Similarity	95.7%;	Pred. NO. 0;	Mismatches 17;	Indels 53;
Matches 1553;	Conservative	0;	Gaps 2;	
QY	2	GAAATTTGCTTTGGGATGAAGCTTTGCAGCCTTTGCAGTCTTTGTACCCATTGTTCTCTT	61	Sequence 9, Appli
DB	1	GAAATTTGCTTTGGGATGAAGCTTTGCAGCCTTTGCAGTCTTTGTACCCATTGTTCTCTT	60	Sequence 13, Appli
QY	62	CTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAAGTTCTAGTGTCTTCTTAGAAC	121	Sequence 11, Appli
DB	61	CTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGGCCAAAGTTCTAGTGTCTTCTTAGAAC	120	Sequence 7, Appli
QY	122	CTCTAGGCAAGTTCAAGTTCTACAGATCTTACTACAAATATGAGATGTTCTCTGGCA	181	Sequence 3, Appli
DB	121	CTCTAGGCAAGTTCAAGTTCTACAGATCTTACTACAAATATGAGATGTTCTCTGGCA	180	Sequence 11, Appli
QY	182	GCCGGTAAACAGCTGACCTTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGATC	241	Sequence 5, Appli
DB	181	GCCGGTAAACAGCTGACCTTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGATC	240	Sequence 7, Appli
QY	242	TGATGTCGAATGTGAAGCCCATTTAAATGTAGCGGAATTTCCATGAGTGTCTTGCT	301	Sequence 3, Appli
DB	241	TGATGTCGAATGTGAAGCCCATTTAAATGTAGCGGAATTTCCATGAGTGTCTTGCT	300	Sequence 1, Appli
QY	302	GGCAGACGTGGAGATCTTATTCAACAGCAGATTTTCAACAGCAGTCAAGTCCCGGAGC	361	Sequence 9, Appli
DB	301	GGCAGATGTGAAGATCTTATTCAACAGCAGATTTTCAACAGCAGTCAAGTCCCGGAGC	360	Sequence 13, Appli
QY	362	CTCCGATCGTACTATGAACAGTATCACTCACTAAATGAATCTATTTTGGATAGATTT	421	Sequence 11, Appli

Db 361 CTCGCATCGTACTATGAAAGATGATCACTCACTAAATGAATCTATTCTTGGATAGAAAT 420  
Qy 422 TATACTGAGAGGATCCTGATATGCTTTACAAAAATCCACATTTGGATCCTCATTTGAGAA 481  
Db 421 TATACTGAGAGGATCCTGATATGCTTTACAAAAATCCACATTTGGATCCTCATTTGAGAA 480  
Qy 482 GTAGCCACTCTATGTTTAAAGGTTCTGGAAGAAACAAACAGCCAAATGCGCATATG 541  
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Qy 542 GATTGACTGTGGAATCCATGCGAGAGATGATCTCTCTGCTTTCTGCTTGTGTTTCAT 601  
Db 541 GATTGACTGTGGAATCCATGCGAGAGATGATCTCTCTGCTTTCTGCTTGTGTTTCAT 600  
Qy 602 AGGCCATAATCGAATGTGGAAGAAACCGTTCTTTCTATCGCAACAATCATTTGCATCGG 661  
Db 601 AGGCCATAATCGAATGTGGAAGAAACCGTTCTTTCTATCGCAACAATCATTTGCATCGG 660  
Qy 662 AACAGACTGAATAGCAACTTTGTTCTCAACACCTGTTGAGGAAGTGCATCCAGTTC 721  
Db 661 AACAGACTGAATAGCAACTTTGTTCTCAACACCTGTTGAGGAAGTGCATCCAGTTC 720  
Qy 722 CTATGCTCGAAACCTACTCTGGACTTTATCTCTGAGTCAGAACAGAGTGAAGGCACT 781  
Db 721 CTATGCTCGAAACCTACTCTGGACTTTATCTCTGAGTCAGAACAGAGTGAAGGCACT 780  
Qy 782 GGCTAGTTTCTTGAGAGAAATATCAACACAGATTAAGCATATCATGATGCATTCATA 841  
Db 781 GGCTAGTTTCTTGAGAGAAATATCAACACAGATTAAGCATATCATGATGCATTCATA 840  
Qy 842 CTCGCAGATATAGTTTCCATATCTATACAGAGTAAAGCAAGCAACCATGAGGA 901  
Db 841 CTCGCAGATATAGTTTCCATATCTATACAGAGTAAAGCAAGCAACCATGAGGA 900  
Qy 902 ACTGCTCTAGTACGAGTGAAGAGTTCGCTGCTATTGACAAAACTAGTAAAAATACAG 961  
Db 901 ACTGCTCTAGTACGAGTGAAGAGTTCGCTGCTATTGAGAAATTAGTAAAAATACAG 960  
Qy 962 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATG 1021  
Db 961 GTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATG 1020  
Qy 1022 GATCTATGATTTGGGCATCAATATTCGT----- 1050  
Db 1021 GATCTATGATTTGGGCATCAATATTCGTTTACAAATGAACTTCGAGATACGGGCACATA 1080  
Qy 1051 -----TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGT 1089  
Db 1081 CGGATTTCTGCTGCGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGT 1140  
Qy 1090 CTCTAAATAGCTTGGCATGTCATAGGAATGTTTAAATGCCCTGATTTATCATCTTCTGC 1149  
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Qy 1150 TTCCGTATTTAAATTTACTGATTCAGCAAGCAACAAATCAATGTATCAGATTTATTTAA 1209  
Db 1201 TTCCGTATTTAAATTTACTGATTCAGCAAGCAACAAATCAATGTATCAGATTTATTTAA 1260  
Qy 1210 GTTTTATCCGTAGTTTGTATAAAGATTTTCTATTTCTGTTCTGTGAGAACCTTAA 1269  
Db 1261 GTTTTATCCGTAGTTTGTATAAAGATTTTCTATTTCTGTTCTGTGAGAACCTTAA 1320  
Qy 1270 TAAGTGCTACTTTGGCCATTAAGGCAGACTAGGGTTCATGCTTTTACCCCTTTAAAAAA 1329  
Db 1321 TAAGTGCTACTTTGGCCATTAAGGCAGACTAGGGTTCATGCTTTTACCCCTTT-AAAAA 1379  
Qy 1330 AATTGTAAGCTAGTTAGTACCTACTTTTCTTGATTTTTCGACGTTTCTAGCCATCTC 1389  
Db 1380 AATTGTAAGCTAGTTAGTACCTACTTTTCTTGATTTTTCGACGTTTCTAGCCATCTC 1439  
Qy 1390 AAGCAACTTTTCGACGTTTTCAGTACCATCTCAAGCAAGTTTAAATCAAAAGATCATCTCAG 1449  
Db 1440 AAGCAAGTTTTCGACGTTTTCAGTACCATCTCAAGCAAGTTTAAATCAATGATCATCTCAG 1499

Qy 1450 CTGATCATTTGGATCCTACTCAACAAAGCAAGGTTGTCAGAAAGTACATTTAAAGATTTCT 1509  
Db 1500 CTGATCATTTGGATCCTACTCAACAAAGCAAGGTTGTCAGAAAGTACATTTAAAGATTTCT 1559  
Qy 1510 GCTCCAAATTTCAATAAATTTCTTCTTCTCCCTTTAAAAAATAAAAAAAAAAAAAA 1569  
Db 1560 GCTCCAAATTTCAATAAATTTCTTCTTCTTCTTCTTAAAAAATAAAAAAAAAAAAAA 1619  
Qy 1570 AAA 1572  
Db 1620 ATA 1622

## RESULT 2

US-07-649-591B-2  
; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: hybridization probe  
; LOCATION: 133 to 178  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: potential clip site  
; LOCATION: 380 to 382  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: signal sequence  
; LOCATION: 41 to 106  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; US-07-649-591B-2

Query Match

87.2%; Score 1372; DB 1; Length 1749;

Beet Local Similarity 90.3%; Pred. No. 0;		Matches 1558; Conservative 0; Mismatches 5; Indels 163; Gaps 2;	
Qy	1	AGAAAAATGCTGTTGGGATGAAGCTTTGCGAGCTTGGAGCTTGTGACCCATTGTTCTCT	60
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Qy	61	TCCTGAGCAGCATGCTCTTCCGTTTCCAGAGTGCCCAAGTTCTAGCTGCTCTTCTTAGAA	120
Db	84	TCCTGAGCAGCATGCTCTTCCGTTTCCAGAGTGCCCAAGTTCTAGCTGCTCTTCTTAGAA	143
Qy	121	CCTTAGGCAAGTTCAAGTTCTACAGAACTTTACTACAAATATGAGATTGTTCTTGGC	180
Db	144	CCTTAGGCAAGTTCAAGTTCTACAGAACTTTACTACAAATATGAGATTGTTCTTGGC	203
Qy	181	AGCCGGTAAACAGCTGACCTTTATGTAAGAAAAAACAAGTCCATTTTTTGTAAATGCAT	240
Db	204	AGCCGGTAAACAGCTGACCTTTATGTAAGAAAAAACAAGTCCATTTTTTGTAAATGCAT	263
Qy	241	CTGATGTCGAAATGTGAAAGCCCAATTTAAATGTGAGCGGAATTTCCATGCAAGTCTTGC	300
Db	264	CTGATGTCGAAATGTGAAAGCCCAATTTAAATGTGAGCGGAATTTCCATGCAAGTCTTGC	323
Qy	301	TGGCAGAGCTGGAAGATCTTATTTCAACAGCAGATTTTCAACGACACAGTCAGCCCCGAG	360
Db	324	TGGCAGAGCTGGAAGATCTTATTTCAACAGCAGATTTTCAACGACACAGTCAGCCCCGAG	383
Qy	361	CTTCGGCATCGTACTATGAAACAGTATCACTCACTAAATGAAATCTATTTCTGGATAGAT	420
Db	384	CTTCGGCATCGTACTATGAAACAGTATCACTCACTAAATGAAATCTATTTCTGGATAGAT	443
Qy	421	TTATAACTGAGAGCATCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTTCAGA	480
Db	444	TTATAACTGAGAGCATCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTTCAGA	503
Qy	481	AGTACCCACTCTATGTTTTTAAAGTTTCTGGAAGAAGAACAAACAGCCAAAAATGCCATAT	540
Db	504	AGTACCCACTCTATGTTTTTAAAGTTTCTGGAAGAAGAACAAACAGCCAAAAATGCCATAT	563
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Qy	601	TAGGCCAT-----	608
Db	624	TAGGCCATATAACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGGCTTG	683
Qy	609	-----A	609
Db	684	TGGATTTCTATGTTATGCGGTGGTTAAATGTGGACGGTTATGACTACTCATGGAAAAAGA	743
Qy	610	ATCGAATGTGGAGAAGAACGGTTCTTTCTATGCGAACAATCATTTGATCGGAACAGACC	669
Db	744	ATCGAATGTGGAGAAGAACGGTTCTTTCTATGCGAACAATCATTTGATCGGAACAGACC	803
Qy	670	TGAATAGCAACTTTGCTCTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCT	729
Db	804	TGAATAGCAACTTTGCTCTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCT	863
Qy	730	CGGAAACCTACTGTGGACTTTTATCCTGAGTCAGAACCCAGAGTGAAGCGAGTGCTAGTT	789
Db	864	CGGAAACCTACTGTGGACTTTTATCCTGAGTCAGAACCCAGAGTGAAGCGAGTGCTAGTT	923
Qy	790	TCCTGAGAAGAAATATCAACAGATTTAAGCATACATCAGCATGCTATCTATCTCCAGC	849
Db	924	TCCTGAGAAGAAATATCAACAGATTTAAGCATACATCAGCATGCTATCTATCTCCAGC	983
Qy	850	ATATAGTGTTCCTATTTCTTATACAGAACTAAAGAACCAAGACCATGAGAACTGTCTC	909
Db	984	ATATAGTGTTCCTATTTCTTATACAGAACTAAAGAACCAAGACCATGAGAACTGTCTC	1043
Qy	910	TAGTAGCAGTGGAAGCAGTTCGTGCTATTGACAAATAGTAAAAATACCAGGTATACAC	969

Db	1044	TAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC	1103
Qy	970	ATGCGCATGCTCAGAAACCTTATACCTAGCTCCTGAGGTGGGACGATTGATCTATG	1029
Db	1104	ATGCGCATGCTCAGAAACCTTATACCTAGCTCCTGAGGTGGGACGATTGATCTATG	1163
Qy	1030	ATTGCGCATCAAAATATTGCT-----	1050
Db	1164	ATTGCGCATCAAAATATTGCTTTTACAATTTGAATCTCGAGATACGGGCACATACGGATTCT	1223
Qy	1051	-----TTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGCTGTCTTAAAA	1097
Db	1224	TGCTGCGGAGCGCTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGCTGTCTTAAAA	1283
Qy	1098	TAGCTTGGCATGTCTATTAGGAATGTTTAAATGCCCTGATTTTATCATTTCTGCTTCCGTAT	1157
Db	1284	TAGCTTGGCATGTCTATTAGGAATGTTTAAATGCCCTGATTTTATCATTTCTGCTTCCGTAT	1343
Qy	1158	TTTAAATTTACTGATTTCCAGCAAGACCAAAATCATTTGTATCAGATTTATTTTAAAGTTTATC	1217
Db	1344	TTTAAATTTACTGATTTCCAGCAAGACCAAAATCATTTGTATCAGATTTATTTTAAAGTTTATC	1403
Qy	1218	CGTAGTTTGTATAAAAAGATTTTCTATTCCTTGGTTCTGTGAGAACCTTAATAAGTCT	1277
Db	1404	CGTAGTTTGTATAAAAAGATTTTCTATTCCTTGGTTCTGTGAGAACCTTAATAAGTCT	1463
Qy	1278	ACTTTCGCATTAGGCAGAGCTAGGGTTTCATGCTTTTACCTTTTAAACCAAAATTTGTA	1337
Db	1464	ACTTTCGCATTAGGCAGAGCTAGGGTTTCATGCTTTTACCTTTTAAACCAAAATTTGTA	1523
Qy	1338	AGCTTAGTTTACCTACTTTTCTTTGATTTTTCGACGTTTTCGACATCTCAAGCAACT	1397
Db	1524	AGCTTAGTTTACCTACTTTTCTTTGATTTTTCGACGTTTTCGACATCTCAAGCAACT	1583
Qy	1398	TTGAGGTTTGTAGCTAGCCATCTCAAGCAAGTTTTAAATCAAGATCATCTCAGCTGATCAT	1457
Db	1584	TTGAGGTTTGTAGCTAGCCATCTCAAGCAAGTTTTAAATCAAGATCATCTCAGCTGATCAT	1643
Qy	1458	TGATCCTTACTCAACAAAAGGAGGTGTCAGAGTACATTAAGATTTTCTCTCCAAA	1517
Db	1644	TGATCCTTACTCAACAAAAGGAGGTGTCAGAGTACATTAAGATTTTCTCTCCAAA	1703
Qy	1518	TTTTCAATAAATTTCTTCTTTTAAACCAAAATTTTAAACCAAAATTTTCTCTCCAAA	1563
Db	1704	TTTTCAATAAATTTCTTCTTTTAAACCAAAATTTTAAACCAAAATTTTCTCTCCAAA	1749

RESULT 3  
US-08-277-540-2  
; Sequence 2, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Dryna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727



; Sequence 2, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-430-787A-2

Query Match 87.2%; Score 1372; DB 1; Length 1749;  
Best Local Similarity 90.3%; Pred. No. 0;  
Matches 1558; Conservative 0; Mismatches 5; Indels 163; Gaps 2;  
  
Qy 1 AGAAAAATGCTGGGATGAAGCTTTTCAGCCTTGCGAGCTCTTGATACCCATTGTTCTCT 60  
Db 24 AGAAAAATGCTGGGATGAAGCTTTTCAGCCTTGCGAGCTCTTGATACCCATTGTTCTCT 83  
  
Qy 61 TCTGTGAGCAGCATGCTTCTCGCGTTCCAGAGTGGCCAAAGTCTAGCTGCTCTTCTAGAA 120  
Db 84 TCTGTGAGCAGCATGCTTCTCGCGTTTCAGAGTGGCCAAAGTCTAGCTGCTCTTCTAGAA 143  
  
Qy 121 CCTCTAGGCAAGTTCAAGTCTTACAGAACTTCTACTACAAACATATGAGATTGTTCTCTGGC 180  
Db 144 CCTCTAGGCAAGTTCAAGTCTTACAGAACTTCTACTACAAACATATGAGATTGTTCTCTGGC 203  
  
Qy 181 AGCCGGTAACAGCTGACCTTTATGGAAGAAAAACAAGTCCATTTTTTTGTAAATGCAT 240  
Db 204 AGCCGGTAACAGCTGACCTTTATGGAAGAAAAACAAGTCCATTTTTTTGTAAATGCAT 263  
  
Qy 241 CTGATGCGCAATGTGAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTGTCTTGC 300  
Db 264 CTGATGCGCAATGTGAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTGTCTTGC 323

Qy 301 TGGCAGACGTGGAAGATCTTTATTTCAACAGCAGATTTTCCAAACGACACAGTCCAGCCCCGAG 360  
Db 324 TGGCAGACGTGGAAGATCTTTATTTCAACAGCAGATTTTCCAAACGACACAGTCCAGCCCCGAG 383  
  
Qy 361 CTCTCCGATCGTACTATGAACAGTATCATCTCACTAAATGAAATCTATTCTTGGATGAAT 420  
Db 384 CTCTCCGATCGTACTATGAACAGTATCATCTCACTAAATGAAATCTATTCTTGGATGAAT 443  
  
Qy 421 TTATAACTGAGAGGCATCTCTGATATGTTTACAAAAATCCACATTTGGATCTCTATTTCGAG 480  
Db 444 TTATAACTGAGAGGCATCTCTGATATGTTTACAAAAATCCACATTTGGATCTCTATTTCGAG 503  
  
Qy 481 AGTACCCACTCTATGTTTAAAGGTTTCTGGAAGAAACAAACAGCCAAATAATGCCATAT 540  
Db 504 AGTACCCACTCTATGTTTAAAGGTTTCTGGAAGAAACAAACAGCCAAATAATGCCATAT 563  
  
Qy 541 GGAATGACTGTGGAATCCATGCGCAGAGAAATGGATCTCTCTCTGCTTCTGCTTGTGGTTCA 600  
Db 564 GGAATGACTGTGGAATCCATGCGCAGAGAAATGGATCTCTCTCTGCTTCTGCTTGTGGTTCA 623  
  
Qy 601 TAGGCCAT ----- 608  
Db 624 TAGGCCATATACTCAATTTCTATGGGATATAGGGCAATATACCAATCTCTGAGGGCTTG 683  
  
Qy 609 -----A 609  
Db 684 TGGATTTCTATGTTATGCCGGTGGTTAAATGTGGACGGTTATGACTACTCATCGAAAAAGA 743  
  
Qy 610 ATCGAATGTGGAGAAAGAACCGTTCTTTTCTATCGGAACAATCATTTGTCATCGGAACAGACC 669  
Db 744 ATCGAATGTGGAGAAAGAACCGTTCTTTTCTATCGGAACAATCATTTGTCATCGGAACAGACC 803  
  
Qy 670 TGAATAGCAACTTGTCTCCAAACACTGTTGTCAGGAAGTGCATCCAGTTCCTCATGCT 729  
Db 804 TGAATAGGAACCTTGTCTCCAAACACTGTTGTCAGGAAGTGCATCCAGTTCCTCATGCT 863  
  
Qy 730 CGGAAACCTACTCTGGACTTTTATCTGAGTCAGAACCCAGAAAGTGAAGGCAAGTGGCTAGTT 789  
Db 864 CGGAAACCTACTCTGGACTTTTATCTGAGTCAGAACCCAGAAAGTGAAGGCAAGTGGCTAGTT 923  
  
Qy 790 TCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGTCATTCATCTCCAGC 849  
Db 924 TCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGTCATTCATCTCCAGC 983  
  
Qy 850 ATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAAGTGTCTC 909  
Db 984 ATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGGAAGTGTCTC 1043  
  
Qy 910 TAGTAGCCAGTGAAGCAGTTCTGTGCTATTGACAAAAACTAGTAAAAATACCAGGTATACAC 969  
Db 1044 TAGTAGCCAGTGAAGCAGTTCTGTGCTATTGAGAAAACTAGTAAAAATACCAGGTATACAC 1103  
  
Qy 970 ATGGCAATGGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTTGATCTATG 1029  
Db 1104 ATGGCAATGGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTTGATCTATG 1163  
  
Qy 1030 ATTTGGGCATCAATATTCGT ----- 1050  
Db 1164 ATTTGGGCATCAATATTCGTTTTACAAATTTGAACTTTCAGATACGGGCACATACGGATTCT 1223  
  
Qy 1051 -----TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGGTGTCTCTAAAAA 1097  
Db 1224 TGCTGCGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGGTGTCTCTAAAAA 1283  
  
Qy 1098 TAGCTTGGCATGTCATTTAGGAATGTTTAAATGCCCTGATTTTATCATTTCTGCTCCGTAT 1157  
Db 1284 TAGCTTGGCATGTCATTTAGGAATGTTTAAATGCCCTGATTTTATCATTTCTGCTCCGTAT 1343  
  
Qy 1158 TTTTAAATTTACTGATCCAGCAAGCAAAATCATTTGATCAGATTATTTTAAAGTTTATC 1217  
Db 1344 TTTTAAATTTACTGATCCAGCAAGCAAAATCATTTGATCAGATTATTTTAAAGTTTATC 1403  
  
Qy 1218 CGTAGTTTTGATAAAAGATTTTCTTATTCCTTCTGTTCTGTCAGAGAACCTTAATAAGTGCT 1277



Db 1404 CGTAGTTTGGATAAAGATTTTCCTATTCCTTGGTCTGTGACGAACTTAATAGTGCT 1463  
Qy 1278 ACTTTGGCATTAAAGCAGACTAGGGTTCATGCTCTTTTACCTTTTAAACCAATTTGTA 1337  
Db 1464 ACTTTGGCATTAAAGCAGACTAGGGTTCATGCTCTTTTACCTTTTAAACCAATTTGTA 1523  
Qy 1338 AAGTCTAGTTACCTACTCTTTCTTTGATTTTTCGACGTTTGAAGTCCATCTCAAGCACT 1397  
Db 1524 AAGTCTAGTTACCTACTCTTTCTTTGATTTTTCGACGTTTGAAGTCCATCTCAAGCACT 1583  
Qy 1398 TTCCAGCTTTGACTAGGCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCAT 1457  
Db 1584 TTCCAGCTTTGACTAGGCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCAT 1643  
Qy 1458 TGGATCTCTACTCAACAAAGGAAGGGTGGTCAGAGTACATTTAAAGATTTTCTGCTCCAAA 1517  
Db 1644 TGGATCTCTACTCAACAAAGGAAGGGTGGTCAGAGTACATTTAAAGATTTTCTGCTCCAAA 1703  
Qy 1518 TTTTCAATAAATTTCTTCTCTCTCTTTTAAACCAATTTTAAACCAATTTTCTGCTCCAAA 1563  
Db 1704 TTTTCAATAAATTTCTTCTCTCTCTTTTAAACCAATTTTAAACCAATTTTCTGCTCCAAA 1749

RESULT 5

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P.  
; AUTHORS: Henzel, William  
; AUTHORS: Drayna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
; TITLE: from Human Plasma

JOURNAL: J. Biol. Chem.  
VOLUME: 266  
ISSUE: 32  
PAGES: 21833-21838  
DATE: No. 5985562 15-1991  
US-08-869-057-1  
Query Match 58.4%; Score 918; DB 2; Length 1272;  
Best Local Similarity 86.8%; Pred. No. 8.2e-224;  
Matches 1104; Conservative 0; Mismatches 5; Indels 163; Gaps 2;  
Qy 18 ATGAAGCTTTGCAAGCTTGCAGTCTTGTACCCATTTGTTCTTCTGTGTGAGCAGCATGTC 77  
Db 1 ATGAAGCTTTGCAAGCTTGCAGTCTTGTACCCATTTGTTCTTCTGTGTGAGCAGCATGTC 60  
Qy 78 TTCGCGTTTCCAGAGTGGCGCAAGTTCTAGTCTGCTTCTTCTAGAACCTCTAGGCAAGTTCAA 137  
Db 61 TTCGCGTTTCCAGAGTGGCGCAAGTTCTAGTCTGCTTCTTCTAGAACCTCTAGGCAAGTTCAA 120  
Qy 138 GTTCTACAGAACTCTTACTACACATATGATGATTTGTTCTCTGGCAGCGGTAAACAGCTGAC 197  
Db 121 GTTCTACAGAACTCTTACTACACATATGATGATTTGTTCTCTGGCAGCGGTAAACAGCTGAC 180  
Qy 198 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTGTAATGCAATCTGATGTCGACAAATGTG 257  
Db 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTGTAATGCAATCTGATGTCGACAAATGTG 240  
Qy 258 AAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTCTTGTCTGGCAGACGTTGGAAGAT 317  
Db 241 AAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTCTTGTCTGGCAGACGTTGGAAGAT 300  
Qy 318 CTTATTCAACAGCAGATTTTCCAAACGACACAGTCCAGCCCGGAGCTCCCGCATCGTACTAT 377  
Db 301 CTTATTCAACAGCAGATTTTCCAAACGACACAGTCCAGCCCGGAGCTCCCGCATCGTACTAT 360  
Qy 378 GAACAGTATCACTCACTAAATGAAATCTTCTTGTGATGAAATTTTATACTGAGAGCAT 437  
Db 361 GAACAGTATCACTCACTAAATGAAATCTTCTTGTGATGAAATTTTATACTGAGAGCAT 420  
Qy 438 CTTGATATGCTTACAAAATCCACATTCATCTTGTGAGAGTACCCACATCTATGTT 497  
Db 421 CTTGATATGCTTACAAAATCCACATTCATCTTGTGAGAGTACCCACATCTATGTT 480  
Qy 498 TTAAGGTTTCTGAAAAGAAACAAACAGCCAAATGCAATGGAATTTGATCTGGAATC 557  
Db 481 TTAAGGTTTCTGAAAAGAAACAAACAGCCAAATGCAATGGAATTTGATCTGGAATC 540  
Qy 558 CATGCCAGAGAAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAT----- 608  
Db 541 CATGCCAGAGAAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAAATCTCAA 600  
Qy 609 ----- 608  
Db 601 TTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATG 660  
Qy 609 -----AATCGAATGTGAGAAAG 626  
Db 661 CCGGTGGTTAATGTGGACGGTTATGACTTCTATGAAAAGAAATCGAATGTGAGAAAG 720  
Qy 627 AACCGTTCTTTTCTATGCGAAACAATTCATTCGGAACAGACCTGAAATAGCAACTTTGTC 686  
Db 721 AACCGTTCTTTTCTATGCGAACAATTCATTCGGAACAGACCTGAAATAGCAACTTTGCT 780  
Qy 687 TCCAAACACTGGTGTGAGGAGGTGCATTCAGTTCCTCATGCTCGGAAACCTACTGTGGA 746  
Db 781 TCCAAACACTGGTGTGAGGAGGTGCATTCAGTTCCTCATGCTCGGAAACCTACTGTGGA 840  
Qy 747 CTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGAGTGGCTAGTTCCTTGTGAGAAATATC 806  
Db 841 CTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGAGTGGCTAGTTCCTTGTGAGAAATATC 900  
Qy 807 AACAGATTAAAGCATACATCAGCATGCTTTCATATCTCCAGCATATAGTGTTCATAT 866  
Db 807 AACAGATTAAAGCATACATCAGCATGCTTTCATATCTCCAGCATATAGTGTTCATAT



Db 901 AACGAGATTAAAGCATATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 960  
Qy 867 TCCTATACAGCAAGTAAAGCAAGCAAGCATGAGAACTGCTCTAGTAGCAGTGAAGCA 926  
Db 961 TCCTATACAGCAAGTAAAGCAAGCAAGCATGAGAACTGCTCTAGTAGCAGTGAAGCA 1020  
Qy 927 GTTCGTGCTATGACAAAACCTAGTAAATAACAGGTATACACATGCCATGGCTCAGAA 986  
Db 1021 GTTCGTGCTATGAGAAAACCTAGTAAATAACAGGTATACACATGCCATGGCTCAGAA 1080  
Qy 987 ACCTATACCTAGTCTCTGGAGTGGGACGATTTGGATCTATGATTTGGGCATCAATAT 1046  
Db 1081 ACCTATACCTAGTCTCTGGAGTGGGACGATTTGGATCTATGATTTGGGCATCAATAT 1140  
Qy 1047 TCCT-----TTAC 1054  
Db 1141 TCGTTTACATTGAATTCGAGATACGGGCACATACGATTCCTGTCGGGAGCGTTAC 1200  
Qy 1055 ATCAAAACCCACCTAGAGAGCTTTTCCGCTGCTCTCTAAATPAGCTTGGCATGTCAAT 1114  
Db 1201 ATCAAAACCCACCTAGAGAGCTTTTCCGCTGCTCTCTAAATPAGCTTGGCATGTCAAT 1260  
Qy 1115 AGGAATCTTTAA 1126  
Db 1261 AGGAATCTTTAA 1272  
RESULT 6  
US-09-813-133A-3  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3  
Query Match 30.4%; Score 478.6; DB 4; Length 55827;  
Best Local Similarity 98.0%; Pred. No. 1.9e-111;  
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
Qy 1051 TTACATCAAAACCCACCTAGAGAGCTTTTCCGCTGCTCTCTAAATPAGCTTGGCATGT 1110  
Db 53334 TTACATCAAAACCCACCTAGAGAGCTTTTCCGCTGCTCTCTAAATPAGCTTGGCATGT 53393  
Qy 1111 CATTAGGAATGTTTAAATGCCCTGATTTTATCTCTGCTTCCGCTATTTTAAATTTACTGA 1170  
Db 53394 CATTAGGAATGTTTAAATGCCCTGATTTTATCTCTGCTTCCGCTATTTTAAATTTACTGA 53453  
Qy 1171 TTCAGCAAGCAACCAATCATGTATCATGATTAATTTTAAAGTTTATCCGTAAGTTTGAATA 1230  
Db 53454 TTCAGCAAGCAACCAATCATGTATCATGATTAATTTTAAAGTTTATCCGTAAGTTTGAATA 53513  
Qy 1231 AAAGATTTTCTATTCCTGCTGTCGAGAGACCTTAATAGTGCCTACTTGGCATTA 1290  
Db 53514 AAAGATTTTCTATTCCTGCTGTCGAGAGACCTTAATAGTGCCTACTTGGCATTA 53573  
Qy 1291 GGCAGACTAGGTTTCATGCTTTTTTACCTTTTAAATAAAATTTGTAAGTCTAGTTACC 1350  
Db 53574 GGCAGACTAGGTTTCATGCTTTTTTACCTTTTAAATAAAATTTGTAAGTCTAGTTACC 53632  
Qy 1351 TACTTTTTTCTGATTTTCAGCGTTTTCAGTTCATCTCAAGCAACTTTCGACGTTTGAC 1410

Db 53633 TACTTTTTTCTGATTTTCGACGTTTTCGACGTTTTCGACGTTTTCGACGTTTTCGAC 53692  
Qy 1411 TAGCCATCTCAAGCAAGTTTTAAATCAAAAGATCATCTCAGCTGATCATTTGGATCTCTACTCA 1470  
Db 53693 TAGCCATCTCAAGCAAGTTTTAAATCAATGATCATCTCAGCTGATCATTTGGATCTCTACTCA 53752  
Qy 1471 AAAAAAGGAGGTTGGTGCAGAGTACATTAAGATTTCTCTCCAAATTTTCAATAAAT 1530  
Db 53753 AAAAAAGGAGGTTGGTGCAGAGTACATTAAGATTTCTCTCCAAATTTTCAATAAAT 53812  
Qy 1531 TCTTCTCTCTCTTTAAAAA 1555  
Db 53813 TCTGCTTGTGCTTTTAAATAACAA 53837  
RESULT 7  
US-08-782-760-5  
; Sequence 5, Application US/08782760  
; Patent No. 5948668  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Jacob  
; APPLICANT: Fulga, Netta  
; APPLICANT: Mendelovitch, Simona  
; APPLICANT: Gorecki, Marian  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/782,760  
; FILING DATE: 13-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/378,233  
; FILING DATE: 25-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0336/43847  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 927 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..927  
; US-08-782-760-5

Query Match 7.9%; Score 124; DB 2; Length 927;  
Best Local Similarity 57.9%; Pred. No. 5.3e-22;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;  
Qy 613 GAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAATCATTCGATCGGAACAGCTGA 672

Db 362 GAATGTGGAGAAAACCCGCTCTACTATGCTGGAAGTTCTCTGTTGGGTGTAGACCCCA 421  
Qy 673 ATAGCAACTTTGTCTCAAAACACTGGTGTGAGGAAGGTGCATCAGTTCTCATGTCTGG 732  
Db 422 ACAGGAATTTTAATGC---TGGCTGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478  
Qy 733 AAACCTACTGTGACCTTTATCTCTGAGTCAAGACAGAGTGAAGGAGTGGCTAGTTTCT 792  
Db 479 AAATCTTACTGTGGACCAAGCCCAAGAGTCTGAAAAGAGAGCAAAAGGCCCTGGCAGATTCA 538  
Qy 793 TGAGAGAAATATCAACAGATTAAGCATACATCAGCATGCAATTCATATCTCCAGCATTA 852  
Db 539 TCCGCAACACCTTCCACATCAAGGCTTACCTGACCATCCACTCATATCTCAGATGA 598  
Qy 853 TAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGAACTGTCTCTAG 912  
Db 599 TGCTCTACCTTACTCTCTATGACTACAAACTGCTGAGAACTATGAGGAATTTGAATGCC 658  
Qy 913 TAGCCAGTGAAGCAGTTCTGTCTATTGACAAACTAGTAAATACCAAGTATACACATG 972  
Db 659 TGGTGAAGGTGGGCAAGAGGCTTGCC---ACTCTGCAATGGCACCAGTACACATATG 715  
Qy 973 GCCATGCTCAGAACTTATACCTAGTCTCTGAGGTGGGACGATTGGATCTATGATT 1032  
Db 716 GCCCAGAGCTACAACTATCTCTGCTGTGGGGATCTGACGACTGGTCTTATGATC 775  
Qy 1033 TGGGCATCAATATTCCTTTACATCAAAACCCACTGTGAGAGAGCTTTTCCGCGTGTCT 1092  
Db 776 AGGAATCAATATTCCTTTACCTTTGA-ACTCGGGATACAGGCTTCTTTGGCTTTCTC 834

## RESULT 8

PCT-US96-00995-5  
; Sequence 5, Application PC/TUS9600995  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00995  
; FILING DATE: 25-JAN-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 927 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: 1..927  
PCT-US96-00995-5

Query Match 7.9%; Score 124; DB 5; Length 927;  
Best Local Similarity 57.9%; Pred. No. 5.3e-22;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;

Qy 613 GAATGTGGAGAAACCGTTCTTTCTATGCGAACAATCATTCATCGGAACAGACCTGA 672  
Db 362 GAATGTGGAGAAAACCCGCTCTACTATGCTGGAAGTTCTCTGTTGGGTGTAGACCCCA 421  
Qy 673 ATAGCAACTTTGTCTCAAAACACTGGTGTGAGGAAGGTGCATCAGTTCTCATGTCTGG 732  
Db 422 ACAGGAATTTTAATGC---TGGCTGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478  
Qy 733 AAACCTACTGTGACCTTTATCTCTGAGTCAAGACAGAGTGAAGGAGTGGCTAGTTTCT 792  
Db 479 AAATCTTACTGTGGACCAAGCCCAAGAGTCTGAAAAGAGAGCAAAAGGCCCTGGCAGATTCA 538  
Qy 793 TGAGAGAAATATCAACAGATTAAGCATACATCAGCATGCAATTCATATCTCCAGCATTA 852  
Db 539 TCCGCAACACCTTCCACATCAAGGCTTACCTGACCATCCACTCATATCTCAGATGA 598  
Qy 853 TAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGAACTGTCTCTAG 912  
Db 599 TGCTCTACCTTACTCTCTATGACTACAAACTGCTGAGAACTATGAGGAATTTGAATGCC 658  
Qy 913 TAGCCAGTGAAGCAGTTCTGTCTATTGACAAACTAGTAAATACCAAGTATACACATG 972  
Db 659 TGGTGAAGGTGGGCAAGAGGCTTGCC---ACTCTGCAATGGCACCAGTACACATATG 715  
Qy 973 GCCATGCTCAGAACTTATACCTAGTCTCTGAGGTGGGACGATTGGATCTATGATT 1032  
Db 716 GCCCAGAGCTACAACTATCTCTGCTGTGGGGATCTGACGACTGGTCTTATGATC 775  
Qy 1033 TGGGCATCAATATTCCTTTACATCAAAACCCACTGTGAGAGAGCTTTTCCGCGTGTCT 1092  
Db 776 AGGAATCAATATTCCTTTACCTTTGA-ACTCGGGATACAGGCTTCTTTGGCTTTCTC 834

## RESULT 9

US-08-696-139-3  
; Sequence 3, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hershberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-8681  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..921  
US-08-696-139-3

Query Match 7.8%; Score 123.4; DB 1; Length 921;  
Best Local Similarity 56.3%; Pred. No. 7.5e-22;  
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

QY 572 GATCTCTCTGCTTTCGTTGTTGTTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631  
DB 321 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGACCGAATGTGGAGAAAGAACCG 380

QY 532 TTCTTTCTATCGGACCAATCATTCGATCGGACAGACCTGAATAGCAACTTTGTTCTCCAA 691  
DB 381 CTCTACCAATGCTGGAACTACCTGCAATGGCAGACACCCCAACAGAAATTTTGATGCTG 440

QY 692 ACATGCTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGACTTTA 751  
DB 441 G---TGTTGCAACTGGAGCTCTACAGACCCCTCGATGAGACTTCTGTTGATGCTG 497

QY 752 TCCTGAGTCAAGACCAAGTGAAGGAGTGGCTAGTTTCTTGAGAGAAATATCAACCA 811  
DB 498 TGCAGAGTCTGAAAGAGACCAAGGCTGGCTGATTTTATACGCAACCACTCTCTC 557

QY 812 GATTAAAGCATACATCAGCATGCAATCTATCTCCAGCATATAGTTTCCATATTCCTA 871  
DB 558 CATCAAGCATACCTGAGATCCAGTCCACTCATATCAAGATGATATCTTACCCCTTATTCCTA 617

QY 872 TACACGAAGTAAAGCAAGACCAATGAGGAAGTCTCTCTAGTAGCCAGTCAAGCAGTGC 931  
DB 618 TGATTACAACCTCCCGAGACATGCTGATTTGAATTAACCTGGCTAAGCTGCGGTGAA 677

QY 932 TGCTATTGACAAACTAGTAAATATACAGGTATACATATGCGCATGGCTCAGAAACCTT 991  
DB 678 AGAAGTTG---CTACACTGTATGGCACAAGTACACATACGGCCAGGAGCTACACAAT 734

QY 992 ATACCTAGCTCCTGGAGTGGGAGGATTTGATCTATGATTTGGGCATCAATATTCGTT 1051  
DB 735 CTATCTCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAATATTCCTT 794

QY 1052 TACAT 1056  
DB 795 CACCT 799

RESULT 10  
US-08-696-139-1  
Sequence 1, Application US/08696139  
Patent No. 5672496  
GENERAL INFORMATION:  
APPLICANT: Payerman, Jeffrey T.  
APPLICANT: Greenen, David P.  
APPLICANT: Hershberger, Charles L.  
APPLICANT: Larson, Jeffrey L.  
APPLICANT: Sterner, Jane L.  
APPLICANT: Zhang, Haichao  
TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696,139  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,258  
FILING DATE: 16-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-8681  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1215 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1215  
US-08-696-139-1

Query Match 7.8%; Score 123.4; DB 1; Length 1215;  
Best Local Similarity 56.3%; Pred. No. 8.3e-22;  
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

QY 572 GATCTCTCTGCTTTCGTTGTTGTTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631  
DB 615 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGACCGAATGTGGAGAAAGAACCG 674

QY 632 TTCTTTCTATCGGAAACAATCATTTGCATCGGAACAGACCTGAATPAGCAACTTTTGTCTCCAA 691  
DB 675 CTCTACCAATGCTGGAACTACCTGCAATGGCAGACACCCCAACAGAAATTTTGTGATGCTG 734

QY 692 ACATGCTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGACTTTA 751  
DB 735 G---TGTTGCAACAACCTGGAGCTCTACAGACCCCTCGATGAGACTTACTGTGGATCTGC 791

QY 752 TCCTGAGTCAAGACCAAGTGAAGGAGTGGCTAGTTTCTTGAGAGAAATATCAACCA 811  
DB 792 TGCAGAGTCTGAAAGAGACCAAGGCTGGCTGATTTTATACGCAACCACTCTCTCCTC 851

QY 812 GATTAAAGCATACATCAGCATGCAATCTATCTCCAGCATATAGTTTCCATATTCCTA 871  
DB 852 CATCAAGCATACCTGACCATCCACTCATATCAAGATGATATCTTACCCCTTATTCCTA 911

QY 872 TACACGAAGTAAAGCAAGACCAATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCG 931  
DB 912 TGATTACAAACTCCCGAGACCAATGCTGAGTTGAATAACCTGGCTAAGGCTGCGGTGAA 971

QY 932 TGCTATTGACAAACTAGTAAATATACAGGTATACATATGCGCATGGCTCAGAAACCTT 991  
DB 972 AGAAGTTG---CTACACTGTATGGCACAAGTACATATGCGCCCAAGGAGCTACACAAT 1028

QY 992 ATACCTAGCTCCTGGAGTGGGAGGATTTGATCTATGATTTGGGCATCAATATTCGTT 1051

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Db 1029 CTATCCTGCTGCTGGGGCTGTGATGACTGGGCTTATGACCAAGGAATCAAAATATTCCTT 1088
Qy 1052 TACAT 1056
Db 1089 CACCT 1093

RESULT 11
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARGHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

Query Match 6.9%; Score 109; DB 4; Length 1263;
Best Local Similarity 54.4%; Pred. No. 3.9e-18;
Matches 264; Conservative 0; Mismatches 215; Indels 6; Gaps 2;

Qy 572 GATCTCTCCTCTTCTGCTTGTGTTTCATAGGCCAATCGAATGTGGAGAAAGAACCG 631
Db 645 GCTCAATATTGATGGCTACATCTACCTGGACCAAGCCGATTTGGAGAAAGACTCG 704
Qy 632 TTCTTTCTATCGAACATCATTTGCATCGGAACAGACCTGAATAGCAACTTTGTCTCAA 691
Db 705 CTCCACCACATCTGGATCTAGCTGATGGACAGACCCCAACAGAAATTTGATGC--- 761
Qy 692 ACATGGTGTGAGAAAGTGCATCCAGTTCCTCTGCTCGGAACCTTACTGTGCACTTA 751
Db 762 TGGTTGGTGTGAAATTTGGAGGCTCTCGAAACCCCTGTGATGAAATCTACTGTGACCTGC 821
Qy 752 TCCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTCTTTGAGAGAAATATCAACCA 811
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Db 822 CGCAGAGTCTGAAAGGAAACCAAGGCCCTGGCTGATTTTCATCCGCAACAAACTCTCTTC 881
Qy 812 GATTAAGCATCATCATCAGCATGCATTCATCTACCTCCAGCATATAGTGTTCCTATTCCTA 871
Db 882 CATCAAGGCATATCTGACAAATCCACTCGTACTCCCAATGATGATACCTCTTACTCATA 941
Qy 872 TACACGAAGTAAAGCAAAAGACCATGAGCAACTGTCTCTAGTAGCCAGTGAAGCAGTTGC 931
Db 942 TGTTCACAACTCGGTGAGAACAACTGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 1001
Qy 932 TGCTATTGACAAACTAGTAAAAATACCAAGGTATACACATGGCCATGGCTCAGAAACCTT 991
Db 1002 AGAACTTGCC---TCACTGCACGGCACCIAGTAGTACATATGGCCCGGAGCTACAAAT 1058
Qy 992 ATACCTAGCTCCTGGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAATATTCGTT 1051
Db 1059 CTATCCTGCTGCTGGGGGCTCTGACGACGGGCTTATGACCAAGGAATCAGATATTCCTT 1118
Qy 1052 TACAT 1056
Db 1119 CACCT 1123

RESULT 12
US-09-023-655-1020
; Sequence 1020, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1020:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179933
US-09-023-655-1020
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Query Match	6.8%;	Score 107.6;	DB 4;	Length 1622;
Best Local Similarity	55.6%;	Pred. No. 9.7e-10;		
Matches 250;	Conservative 0;	Mismatches 194;	Indels 6;	Gaps 2;
Qy	607	ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATATGCGAAACAATCATTTGCATCGGAACAG	666	
Db	686	AGAACCGCATGTGGAGAAAAAATCGTTCCAGAAGACCAAAACTCCAAATGCATCGGCAC	745	
Qy	667	ACCTGATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCAT	726	
Db	746	ACCTCAACAGGAATTTTAATGCTTCA---TGGAACTCCATTCCTTAACCAACAATGACCCAT	802	
Qy	727	GCTCGGAAACCTACTGTGGAGCTTTTATCCTCGAGTCAGAACCAAGAGTGAAGGCCAGTGGCTA	786	
Db	803	GTGCAGATAACTATCGGGGCTCTGCACCAGATCCGAGAAAGAGACGAAAGCTGTCACTA	862	
Qy	787	GTTTCTTTGAGAAGAAATATCAACAGATTTAAAGCATACATCAGATGCATTCATCTCCC	846	
Db	863	ATTTTCATTAGAAGCCACCTGAATGAAATCAAGGTTTATCATCACTTCCATTCCTACTCCC	922	
Qy	847	AGCATATAGTGTGTTTCCATATTTCTCTATACAGAAAGTAAAGCAAAGACCATGAGGAACTGT	906	
Db	923	AGATGCTATTGTTTCCCTATGGATATACATCAAAACTGCCACCTAACCATGAGGACTTGG	982	
Qy	907	CTCTAGTAGCCAGTGAAGCAGTTGTGCTATTGACAAAACTAGTAAAAATACACAGGTATA	966	
Db	983	CCAAAGTGGCAA---AGATTGGCACTGATGTTCTATCAACTCGATATGAAACCGGTACA	1039	
Qy	967	CACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGAGGTGGGAGCGATTGGATCT	1026	
Db	1040	TCTATGGCCCAATAGATCAACAATTTACCGGATATCAGGTTCTCTTTTAGACTGGGCTT	1099	
Qy	1027	ATGATTGGGCATCAAAATATTCGTTACAT	1056	
Db	1100	ATGACCTGGGCATCAAAACACACATTTGCCT	1129	

RESULT 13

US-08-860-882A-67  
 : Sequence 67, Application US/08860882A  
 : Patent No. 5985281  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
 : APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
 : APPLICANT: TARRAGONA-FIOL, ANTONIO  
 : APPLICANT: RABIN, BRIAN ROBERT  
 : APPLICANT: BOYLE, FRANCIS THOMAS  
 : APPLICANT: HENNAM, JOHN FREDERICK  
 : APPLICANT: BLAKELY, DAVID CHARLES  
 : APPLICANT: MARSHAM, PETER ROBERT  
 : APPLICANT: HEATON, DAVID WILLIAM  
 : APPLICANT: DAVIES, DAVID HOW  
 :  
 : TITLE OF INVENTION: CHEMICAL COMPOUNDS  
 :  
 : NUMBER OF SEQUENCES: 77

**RESULT 14**

RESULT 14  
US-09-011-769A-50  
; Sequence 50, Application US/09011769A  
: Patent No. 6436691

PATENT NO. 6436851  
 GENERAL INFORMATION:  
 APPLICANT: SLATER, Anthony M.  
 BLAKEY, David C.  
 DAVIES, David H.  
 HENNAM, John F.  
 HENNEQUIN, Laurent F.A.  
 MARSHAM, Peter R.  
 DOWELL, Robert I.  
 TITLE OF INVENTION: Chemical Compounds  
 NUMBER OF SEQUENCES: 87  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Pillsbury Madison & Sutro, LLP  
 STREET: 1100 New York Ave., N.W.  
 CITY: Washington  
 STATE: D.C.

```

; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..987
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..987
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-011-769A-50.

Query Match 6.8%; Score 107.4; DB 4; Length 999;
Best Local Similarity 54.2%; Pred. No. 9e-18;
Matches 263; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

Qy 572 GATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
Db 387 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGCGCGATTTTGGAGAAAGACTCG 446

Qy 632 TTCTTTCTATCGGAACCAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTCTCAA 691
Db 447 CTCCACCCATCTGGATCTAGTCTAGCTGCAATTCGACAGACCCCAACAGAAATTTGATGC 503

Qy 812 GATTAAAGCATACATAGCATGCAATTCATCTCCAGCATATAGTGTTCATATTCCTA 871
Db 624 CATCAAGGCATATCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683

Qy 872 TACACGAAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 931
Db 684 TGCTTACAACTCGGTGAGAACAAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAA 743

Qy 932 TGCTATTGACAAAATAGTAAATAATACAGATATACATGGCCATGGCTCAGAAACCTT 991
Db 744 AGAATCTGCC--TCACTGCACCGCACCAAGTACACATATGGCCCGGAGCTACAAAT 800

Qy 992 ATACTAGTCTCTGAGTGGGAGGATGGATCTATGATTTGGGATCAAAATTCGTT 1051
Db 801 CTATCTGCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 860

Qy 1052 TACAT 1056
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Db 861 CACCT 865

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RESULT 15
US-08-860-882A-64
; Sequence 64, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUM
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/23865.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1053 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-860-882A-64
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Query Match 6.8%; Score 107.4; DB 2; Length 1053;
Best Local Similarity 54.2%; Pred. No. 9.2e-18;
Matches 263; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

Qy 572 GATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCATAATCGAATGTGGAGAAAGAACCG 631
Db 387 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGCGCGATTTTGGAGAAAGACTCG 446

Qy 632 TTCTTTCTATCGGAACCAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTCTCAA 691
Db 447 CTCCACCCATCTGGATCTAGTCTAGCTGCAATTCGACAGACCCCAACAGAAATTTGATGC 503

Qy 692 ACATCTGGTGTGAGAAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTTCTGTGAGACTTTA 751
Db 504 TGGTTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGACCTGC 563

Qy 752 TCCTGATCAGACCAAGTGAAGCAATGGCTAGTCTTCTTCTGAGAGAAATATCAACCA 811
Db 564 CGCAGAGTCTGAAAGAGAGACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTTCTCTTC 623
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Qy	812	GATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATATTCCTA	871
Db	624	CATCAAGGCATATCTGACAAATCCACTCGTACTCCAAATGATGATCTACCCTTACTCATA	683
Qy	872	TACACGAAGTAAAGCAAAGACCAATGAGGAACTGTCTTAGTAGCCAGTGAAGCAGTTGG	931
Db	684	TGCTTACAAACTCGGTGAGAACAAATGCTGAGTTGAATGCCCTGCTAAAGCTACTGTGAA	743
Qy	932	TGCTATTGACAAAACTAGTAAAAATACCAAGTATACACATGGCCATGGCTCAGAAACCTT	991
Db	744	AGAACTTGCC---TCACTGACGGCACCAAGTACACATATGGCCCGGAGCTACAACAAT	800
Qy	992	ATACCTAGCTCCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAAAATATTCGTT	1051
Db	801	CTATCCTGTGCTGGGGGCTCTGACGACTGGCTTATGACCAAGGAATCAGATATTCCTT	860
Qy	1052	TACAT	1056
Db	861	CACCT	865

Search completed: October 31, 2004, 00:10:45  
Job time : 159 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1469.8	93.4	1625	9	US-09-813-1133A-1	Sequence 1, Appli
2	1469.8	93.4	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1372	87.2	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1343.8	85.4	1743	16	US-10-115-479-67	Sequence 67, Appl
5	932.8	59.3	1344	16	US-10-115-479-69	Sequence 69, Appl
6	858.8	54.6	1272	15	US-10-379-836-1	Sequence 1, Appli
7	853.8	54.3	1400	9	US-09-925-302-24	Sequence 24, Appl
8	853.8	54.3	1400	10	US-09-925-302-24	Sequence 24, Appl
9	688	43.7	1037	16	US-10-115-479-63	Sequence 63, Appl
10	610.4	38.8	1132	16	US-10-115-479-65	Sequence 65, Appl
11	478.6	30.4	5827	9	US-09-813-1133A-3	Sequence 3, Appli
12	478.6	30.4	5827	14	US-10-212-877-3	Sequence 3, Appli

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QY 182 GCCGGTAACTGACCTTATTTGTAAGAAAAAACAAGTCCATTTTTTGTGTAATGCATC 241
Db 181 GCCGGTAACTGACCTTATTTGTAAGAAAAAACAAGTCCATTTTTTGTGTAATGCATC 240
QY 242 TGATGTCGACAACTGTAAGGCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTGCT 301
Db 241 TGATGTCGACAACTGTAAGGCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTGCT 300
QY 302 GGCAGAGTGAAGATCTTATTTCAACAGCAGATTTCCAACGACACAGTCAGCCGCCGAGC 361
Db 301 GGCAGAGTGAAGATCTTATTTCAACAGCAGATTTCCAACGACACAGTCAGCCGCCGAGC 360
QY 362 CTCGCGATCGTACTATGAAACAGTATCACTCAATAATGAATCTATTTCTTGATAGAAAT 421
Db 361 CTCGCGATCGTACTATGAAACAGTATCACTCAATAATGAATCTATTTCTTGATAGAAAT 420
QY 422 TATAACTGAGAGGATCCTGATATGCTTACAAAATCCACATTCGATCCTCATTTGAGAA 481
Db 421 TATAACTGAGAGGATCCTGATATGCTTACAAAATCCACATTCGATCCTCATTTGAGAA 480
QY 482 GTACCCACTCTATGTTTTAAAGGTTTCTGAAAAAGAACAAACAGCCCAAAAATGCCATATG 541
Db 481 GTACCCACTCTATGTTTTAAAGGTTTCTGAAAAAGAACAAACAGCCCAAAAATGCCATATG 540
QY 542 GATTGACTGTGGAATCCATGCGCAGAGATGGATCTCTCTGCTTTTCTGCTTTGTTGTTTCA 601
Db 541 GATTGACTGTGGAATCCATGCGCAGAGATGGATCTCTCTGCTTTTCTGCTTTGTTGTTTCA 600
QY 602 AGGCCAATCGAATGCGAAGAACCGTTCTTCTATGCGAACAATCATTCATCGATCGG 661
Db 601 AGGCCAATCGAATGCGAAGAACCGTTCTTCTATGCGAACAATCATTCATCGATCGG 660
QY 662 AACAGACTGAATAGCAACTTTGTCTCAAACTGTTGAGGAAGTGTCATCCAGTTC 721
Db 661 AACAGACTGAATAGCAACTTTGTCTCAAACTGTTGAGGAAGTGTCATCCAGTTC 720
QY 722 CTATGCTCGAAACCTTACTGTGACCTTATCTCTGAGTCAGAACAGAGTGAAGGAGT 781
Db 721 CTATGCTCGAAACCTTACTGTGACCTTATCTCTGAGTCAGAACAGAGTGAAGGAGT 780
QY 782 GGCTAGTTCTTGTGAGAGAAATATCAACGATTTAAAGCATACATCAGCATGCAATTCATA 841
Db 781 GGCTAGTTCTTGTGAGAGAAATATCAACGATTTAAAGCATACATCAGCATGCAATTCATA 840
QY 842 CTCCAGCATATAGTGTTCATATTCCTATACAGGAAGTAAAGCAAGACCATGAGGA 901
Db 841 CTCCAGCATATAGTGTTCATATTCCTATACAGGAAGTAAAGCAAGACCATGAGGA 900
QY 902 ACTGCTCTAGTACGCGAGTGAAGCATGCTGCTATTTGACAAACTAGTAAATAACAG 961
Db 901 ACTGCTCTAGTACGCGAGTGAAGCATGCTGCTATTTGAGAAATTTAGTAAATAACAG 960
QY 962 GTATACACATGCGCATGCTCAGAAACCTTATACCTAGTCTCTGAGTGGGACGATG 1021
Db 961 GTATACACATGCGCATGCTCAGAAACCTTATACCTAGTCTCTGAGTGGGACGATG 1020
QY 1022 GATCTATGATTTGGGCATCAATATTCGT ----- 1050
Db 1021 GATCTATGATTTGGGCATCAATATTCGT ----- 1050
QY 1051 -----TTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGTGT 1089
Db 1081 CGGATTTCTGTCGCGGAGCGTTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGTGT 1140
QY 1090 CTCTAAATAGCTTGGCATGTCATTAGGAATGTTTAAATGCCCTGATTTTATCATCTGCG 1149
Db 1141 CTCTAAATAGCTTGGCATGTCATTAGGAATGTTTAAATGCCCTGATTTTATCATCTGCG 1200
QY 1150 TTCGGTATTTTAAATTTACTGATTCAGCAAGACCAAAATCATTTGATCAGATTTATTTAA 1209
Db 1201 TTCGGTATTTTAAATTTACTGATTCAGCAAGACCAAAATCATTTGATCAGATTTATTTAA 1260
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QY 1210 GTTTTATCCGTAGCTTTTGTATAAAGATTTTCCTATTCCTTGGTTCGTGACAGAACCTAA 1269
Db 1261 GTTTTATCCGTAGCTTTTGTATAAAGATTTTCCTATTCCTTGGTTCGTGACAGAACCTAA 1320
QY 1270 TAAAGTGTACTTTTGGCCATTAAAGCAGACTAGGGTTCATGTCTTTTACCCCTTTAAAAAAA 1329
Db 1321 TAAAGTGTACTTTTGGCCATTAAAGCAGACTAGGGTTCATGTCTTTTACCCCTTT-AAAAA 1379
QY 1330 AATTGTAAGAGTCTAGTACCTACTTTTCTTTTGTGATTTTCGAGTTTGACATGCAATCTC 1389
Db 1380 AATTGTAAGAGTCTAGTACCTACTTTTCTTTTGTGATTTTCGAGTTTGACATGCAATCTC 1439
QY 1390 AAGCAACTTTTCGAGTTTGACATGAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACG 1449
Db 1440 AAGCAAGTTTTCGAGTTTGACATGAGCCATCTCAAGCAAGTTTAAATCAATGATCATCTCACG 1499
QY 1450 CTGATCATTTGGAATCTTACTCAACAAAGGAAGGGTGTGTCAGAAAGTACATTTAAAGATTTCT 1509
Db 1500 CTGATCATTTGGAATCTTACTCAACAAAGGAAGGGTGTGTCAGAAAGTACATTTAAAGATTTCT 1559
QY 1510 GCTCCAAATTTTCAATAAATTTCTTCTTCTTAAATAAATAAATAAATAAATAAATAA 1569
Db 1560 GCTCCAAATTTTCAATAAATTTCTTCTTCTTAAATAAATAAATAAATAAATAAATAA 1619
QY 1570 AAA 1572
Db 1620 ATA 1622

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Query Match 93.4%; Score 1469.8; DB 14; Length 1625;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1553; Conservative 0; Mismatches 17; Indels 53; Gaps 2;

QY 2 GAAAAATGCTGTGGGATGAAGCTTTGCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAC 121
Db 1 GAAAAATGCTGTGGGATGAAGCTTTGCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAC 60
QY 62 CTGTGAGCAGCATGTCTTCCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAC 121
Db 61 CTGTGAGCAGCATGTCTTCCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAAC 120
QY 122 CTCTAGCAAGTTCAAGTTCACAGAAATTTTACATCAACATATGAGATGTTCTCTGGCA 181
Db 121 CTCTAGCAAGTTCAAGTTCACAGAAATTTTACATCAACATATGAGATGTTCTCTGGCA 180
QY 182 GCGGTAACAGCTGACCTTATTTGAGGAAABAAACAGTCCATTTTTCGTAATGATC 241
Db 181 GCGGTAACAGCTGACCTTATTTGAGGAAABAAACAGTCCATTTTTCGTAATGATC 240
QY 242 TGATGTGCAAAATGTGAAAGCCCAATTTTAAATGTGAGCGGAATTCATGCAATGCTTCTGCT 301
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Db 241 TGATGTCGACAAATGTGAAAGCCCAATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTGCT 300  
Qy 302 GGCAGAGTGGAGATCTTATTCACAGCAGATTTCCAAAGACAGTGTGACGCCCGGAGC 361  
Db 301 GGCAGAGTGGAGATCTTATTCACAGCAGATTTCCAAAGACAGTGTGACGCCCGGAGC 360  
Qy 362 CTCGGCATCGTACTATGAAACAGTATCACTCACTAAATGAAATCTATTTCTTGGATAGAAAT 421  
Db 361 CTCGGCATCGTACTATGAAACAGTATCACTCACTAAATGAAATCTATTTCTTGGATAGAAAT 420  
Qy 422 TATAACTGAGAGGATCTGATATGCTTACAAAATCCAAATGGAATCTGATCTCAATTTAGAA 481  
Db 421 TATAACTGAGAGGATCTGATATGCTTACAAAATCCAAATGGAATCTGATCTCAATTTAGAA 480  
Qy 482 GTACCCACTCTATGTTTAAAGGTTCTGGAAGAACCAAGCCCAAAATGCCATATG 541  
Db 481 GTACCCACTCTATGTTTAAAGGTTCTGGAAGAACCAAGCCCAAAATGCCATATG 540  
Qy 542 GATTGACTGTGGAATCCATGCCAGAGATGATCTCTCTGCTTTCTGCTTGTGTTTCAT 601  
Db 541 GATTGACTGTGGAATCCATGCCAGAGATGATCTCTCTGCTTTCTGCTTGTGTTTCAT 600  
Qy 602 AGGCATAAATCGAATGTGGAGAAACCGTCTTCTATGCGAACAAATCATTCGATCGG 661  
Db 601 AGGCATAAATCGAATGTGGAGAAACCGTCTTCTATGCGAACAAATCATTCGATCGG 660  
Qy 662 AACAGACTGAAATAGCAACTTGTCTCAACACACTGTTGTGAGGAAGTGCATCCAGTTC 721  
Db 661 AACAGACTGAAATAGCAACTTGTCTCAACACACTGTTGTGAGGAAGTGCATCCAGTTC 720  
Qy 722 CTATGCTCGGAAACCTACTGTGACCTTATCTCTGAGTCAGAACAGAGTGAAGGAGT 781  
Db 721 CTATGCTCGGAAACCTACTGTGACCTTATCTCTGAGTCAGAACAGAGTGAAGGAGT 780  
Qy 782 GGCTAGTCTTCTGAGAGAAATATCAACAGATATTAAGACATACATGACATGCAATTCATA 841  
Db 781 GGCTAGTCTTCTGAGAGAAATATCAACAGATATTAAGACATACATGACATGCAATTCATA 840  
Qy 842 CTCCAGCATATAGTGTTCATATTCCTATACAGGAATTAAGGAAAGAACCATGAGGA 901  
Db 841 CTCCAGCATATAGTGTTCATATTCCTATACAGGAATTAAGGAAAGAACCATGAGGA 900  
Qy 902 ACTGCTCTAGTAGCAGTGAAGCAGTTCGTGCTATTGACAAACTAGTAAATAATACAG 961  
Db 901 ACTGCTCTAGTAGCAGTGAAGCAGTTCGTGCTATTGAGAAAATAGTAAATAATACAG 960  
Qy 962 GTATACATGCGCATGGCTCAGAAACCTTATACCTAGCTCTGAGGAGTGGGACGATG 1021  
Db 961 GTATACATGCGCATGGCTCAGAAACCTTATACCTAGCTCTGAGGAGTGGGACGATG 1020  
Qy 1022 GATCTATGATTTGGGCATCAAAATTTGCTTTTACAAATTTGAATTCGAGATACGGGCACATA 1080  
Db 1021 GATCTATGATTTGGGCATCAAAATTTGCTTTTACAAATTTGAATTCGAGATACGGGCACATA 1080  
Qy 1051 -----TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGGTG 1089  
Db 1081 CGGATTCCTGTCGGGAGCGGTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGGTG 1140  
Qy 1090 CTCTAAATAGCTTGGCATGTCAATAGGAATGTTTAAATGCCCTGATTTTATCATCTGC 1149  
Db 1141 CTCTAAATAGCTTGGCATGTCAATAGGAATGTTTAAATGCCCTGATTTTATCATCTGC 1200  
Qy 1150 TTCCGTAATTTTATTTATCTGATTCAGCAGACCAAAATCAATGTATCAGATTAATTTTAA 1209  
Db 1201 TTCCGTAATTTTATTTACTGATTCAGCAGACCAAAATCAATGTATCAGATTAATTTTAA 1260  
Qy 1210 GTTTTATCCGTAGTTTGAATAAGATTTTCTTATCTCTGTTCTGTCTGAGAGAACCTAA 1269  
Db 1261 GTTTTATCCGTAGTTTGAATAAGATTTTCTTATCTCTGTTCTGTCTGAGAGAACCTAA 1320  
Qy 1270 TAAGTGCTACTTTTGCATTAAGGAGCAGACTAGGGTTCATGTCTTTTACCCCTTTTAAAAAAA 1329  
Db 1321 TAAGTGCTACTTTTGCATTAAGGAGCAGACTAGGGTTCATGTCTTTTACCCCTTTTAAAAAAA 1379

Qy 1330 AATTGTAAAGTCTAGTACTACTTTTCTTTGATTTTTCGACGTTTGACTAGCCATCTC 1389  
Db 1380 AATTGTAAAGTCTAGTACTACTTTTCTTTGATTTTTCGACGTTTGACTAGCCATCTC 1439  
Qy 1390 AAGCAACTTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACG 1449  
Db 1440 AAGCAAGTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAAATCAATGATCATCTCACG 1499  
Qy 1450 CTGATCATTTGGATCTTACTCAACAAAGGAGGTTGTCAGAGTACATTTAAAGATTTCT 1509  
Db 1500 CTGATCATTTGGATCTTACTCAACAAAGGAGGTTGTCAGAGTACATTTAAAGATTTCT 1559  
Qy 1510 GCTCCAAATTTTCAATAAATTTCTTCTCTCTTTTAAAAAATAAATAAATAAATAAATAA 1569  
Db 1560 GCTCCAAATTTTCAATAAATTTCTTCTCTCTTTTAAAAAATAAATAAATAAATAAATAA 1619  
Qy 1570 AAA 1572  
Db 1620 ATA 1622

## RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 4921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Query Match 87.2%; Score 1372; DB 9; Length 1728;  
Best Local Similarity 90.3%; Pred. No. 0;  
Matches 1558; Conservative 0; Mismatches 5; Indels 163; Gaps 2;

Qy 1 AGAAATTTGCTGTGGGATGAAGCTTTGACAGCTTCAGTCTTGTACCCATTTGTTCTCT 60  
Db 3 AGAAATTTGCTGTGGGATGAAGCTTTGACAGCTTCAGTCTTGTACCCATTTGTTCTCT 62  
Qy 61 TCTGTGAGCAGCATGTCTTCGCGTTCCAGTGCGCAAGTTCTAGTGTCTTCTCTAGAA 120  
Db 63 TCTGTGAGCAGCATGTCTTCGCGTTTCAGAGTGCGCAAGTTCTAGTGTCTTCTCTAGAA 122  
Qy 121 CCTCTAGGCAAGTTCAGTCTTACTACAGATCTTACTACACATATGAGATTTCTCTGGC 180  
Db 123 CCTCTAGGCAAGTTCAGTCTTACTACAGATCTTACTACACATATGAGATTTCTCTGGC 182  
Qy 181 AGCCGCTAACAGCTGACCTTTATTTGTAAGAAAAACAAGTCCATTTTTTTGTAATGCAT 240  
Db 183 AGCCGCTAACAGCTGACCTTTATTTGTAAGAAAAACAAGTCCATTTTTTTGTAATGCAT 242  
Qy 241 CTGATGTGCAAAATGTGAAAGCCATTTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGC 300  
Db 243 CTGATGTGCAAAATGTGAAAGCCATTTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGC 302

Qy	301	TGGCAGACGTGGAAAGATCTTTATTCAAACAGCAGATTTTCCAAACGACACAGTCAGTCCGCCCGAG	360
Db	303	TGGCAGACGTGGAAAGATCTTTATTCAAACAGCAGATTTTCCAAACGACACAGTCAGTCCGCCCGAG	362
Qy	361	CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT	420
Db	363	CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAT	422
Qy	421	TTATAACTGAGAGGCATCCTGATGCTTACAAAAATCCCATTTGGATCCTCTATTGAGA	480
Db	423	TTATAACTGAGAGGCATCCTGATGCTTACAAAAATCCCATTTGGATCCTCTATTGAGA	482
Qy	481	AGTACCACCTCTATTGTTTTAAAGTTTCTGGAAAAGAACAAACAGCCAAAATGCCATAT	540
Db	483	AGTACCACCTCTATTGTTTTAAAGTTTCTGGAAAAGAACAAACAGCCAAAATGCCATAT	542
Qy	541	GGATTGACTGGNAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTGTGGTTCA	600
Db	543	GGATTGACTGGNAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTGTGGTTCA	602
Qy	601	TAGGCCAT-----	608
Db	603	TAGGCCATATACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTG	662
Qy	609	-----A	609
Db	663	TGGATTCTTATGTTATGCCGCTGGTTAAATGTGGACGGTTATGACTACTCATGTGAAAAGA	722
Qy	610	ATCGAATGTGGAGAAAGAACCGTTCTTTTCTATGCGAACATTCATTCGATCGGAACAGACC	669
Db	723	ATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACCAATTCATTCGGAACAGACC	782
Qy	670	TGAATAGCAACTTTGCTCTCCAAACACATGCTGTGAGGAAGGTGCATCCAGTTCTCTCATGCT	729
Db	783	TGAATAGCAACTTTGCTTCCAAACACATGCTGTGAGGAAGGTGCATCCAGTTCTCTCATGCT	842
Qy	730	CGGAAACCTACTGTGAGACTTTTATCCTCGAGTCAGAACAGAAAGTGAAGCGCAGTCGCTAGTT	789
Db	843	CGGAAACCTACTGTGAGACTTTTATCCTCGAGTCAGAACAGAAAGTGAAGCGCAGTCGCTAGTT	902
Qy	790	TCTTGAGAGAANAATATCAACACAGATTTAAAGGATACATCAGGATGCAATTCATCTCCAGC	849
Db	903	TCTTGAGAGAANAATATCAACACAGATTTAAAGGATACATCAGGATGCAATTCATCTCCAGC	962
Qy	850	ATATAGTGTTCATATTTCTCTATACAGAGTAAAGCAAGCCATGAGGAACTGTCTC	909
Db	963	ATATAGTGTTCATATTTCTCTATACAGAGTAAAGCAAGCCATGAGGAACTGTCTC	1022
Qy	910	TAGTAGCCAGTGAAGCAGTTCGTCTATTTGACAAAACTAGTAAAAATACCAGGTATACAC	969
Db	1023	TAGTAGCCAGTGAAGCAGTTCGTCTATTTGAGAAAACTAGTAAAAATACCAGGTATACAC	1082
Qy	970	ATGCCCATGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGAGCATGGAATCTATG	1029
Db	1083	ATGCCCATGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGAGCATGGAATCTATG	1142
Qy	1030	ATTTTGGCACAATAATTCGT-----	1050
Db	1143	ATTTTGGCACAATAATTCGTGTTTACAATTTGAGTAACCTTCGAGATAACGGGACATACGGATTTCT	1202
Qy	1051	-----TTACATCAAAACCCACCTGTAGAGAAGCTTTTTCGCGCTGTCTCTAAAA	1097
Db	1203	TGTCGCCGAGCGTTACATCAAACCCACCTGTAGAGAAGCTTTTTCGCGCTGTCTCTAAAA	1262
Qy	1098	TAGCTTGGCATGTCAATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCGTAT	1157
Db	1263	TAGCTTGGCATGTCAATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCGTAT	1322
Qy	1158	TTTTAAATTTACTGATCCAGCAAGCAAAATCATTTGTATCAGATTTATTTTAAAGTTTTATC	1217
Db	1323	TTTTAAATTTACTGATTCAGCAAGCAAAATCATTTGTATCAGATTTATTTTAAAGTTTTATC	1382
Qy	1218	CGTAGTTTTTGATAAAAGATTTTCTCTATTCTCTGCTTCTGTGCAGAGAACCATAAAGTGCT	1277

## RESULT 4

US-10-115-479-67  
: Sequence 67, Application US/10115479

## : Publication No. US20

7	EDUCATION NUMBER: 60/281,657
8	GENERAL INFORMATION:
9	APPLICANT: Li, Li
10	APPLICANT: Gerlach, Valerie L.
11	APPLICANT: Liu, Xiaohong
12	APPLICANT: Miller, Charles E.
13	APPLICANT: Sytek, Kimberly A.
14	APPLICANT: Zerkusen, Bryan D.
15	APPLICANT: Pena, Carol E.A.
16	APPLICANT: Shenoy, Suresh G.
17	APPLICANT: Zhong, Haihong
18	APPLICANT: Smithson, Glendda
19	APPLICANT: Casman, Stacie J.
20	APPLICANT: Boldog, Ferenc L.;
21	APPLICANT: Voss, Edward
22	APPLICANT: Vernet, Corine
23	APPLICANT: MacDougall, John A.
24	APPLICANT: Rastelli, Luca
25	APPLICANT: Anderson, David W.
26	APPLICANT: Zhong, Mei
27	APPLICANT: Mezes, Peter S.
28	APPLICANT: Furtak, Katarzyna
29	APPLICANT: Pattarajan, Meera
30	APPLICANT: Burgess, Catherine E.
31	APPLICANT: Malyanker, Uriel M.
32	APPLICANT: Shimkets, Richard A.
33	APPLICANT: Taupier, Raymond J.
34	APPLICANT: Edinger, Shlomit R.
35	APPLICANT: Mazur, Ann
36	TITLE OF INVENTION: THERAPEUTIC POLY
37	FILE REFERENCE: 21402-322 B (Cura 62)
38	CURRENT APPLICATION NUMBER: US/10/11
39	CURRENT FILING DATE: 2002-11-18
40	PRIOR APPLICATION NUMBER: 60/281,136
41	PRIOR FILING DATE: 2001-04-03
42	PRIOR APPLICATION NUMBER: 60/281,853
43	PRIOR FILING DATE: 2001-04-05
44	PRIOR APPLICATION NUMBER: 60/281,906
45	PRIOR FILING DATE: 2001-04-05
46	PRIOR APPLICATION NUMBER: 60/282,934
47	PRIOR FILING DATE: 2001-04-10
48	PRIOR APPLICATION NUMBER: 60/283,657
49	PRIOR FILING DATE: 2001-04-13
50	PRIOR APPLICATION NUMBER: 60/283,678
51	PRIOR FILING DATE: 2001-04-13
52	PRIOR APPLICATION NUMBER: 60/283,657

PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 67  
LENGTH: 1743  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (20)..(1304)  
US-10-115-479-67

Query Match 85.4%; Score 1343.8; DB 16; Length 1743;  
Best Local Similarity 89.4%; Pred. No. 0;  
Matches 1556; Conservative 0; Mismatches 7; Indels 178; Gaps 3;

Qy 1 AGAAATTTGCTGGTGAAGCTTTGCGAGCTTGCAGTCCCTGTGATCCCATTTCTCT 60  
Db 3 AGAAATTTGCTGGGATGAAGCTTTGCGAGCTTGCAGTCCCTGTGATCCCATTTCTCT 62  
Qy 61 TCTGTAGCAGCATGCTTCTGCGTTCAGAGTGCCCAAGTTCAGTGTCTTCTCTAGAA 120  
Db 63 TCTGTAGCAGCATGCTTCTGCGTTCAGAGTGCCCAAGTTCAGTGTCTTCTCTAGAA 122  
Qy 121 CCTTAGGCAAGTTCAAGTCTTACAGAACTTCTACTCAACATATGAGATTTCTCTGGC 180  
Db 123 CCTTAGGCAAGTTCAAGTCTTACAGAACTTCTACTCAACATATGAGATTTCTCTGGC 182  
Qy 181 AGCGGTAAACAGCTGACCTTTATTTGTGAAGAAAAACCAAGTCCATTTTTTTGTAATGCAT 240  
Db 183 AGCGGTAAACAGCTGACCTTTATTTGTGAAGAAAAACCAAGTCCATTTTTTTGTAATGCAT 242  
Qy 241 CTGATGTGCAATGTGAAGCCCATTTAAATGTGAGCGGAATTCAGTGTCTTCTGTC 300  
Db 243 CTGATGTGCAATGTGAAGCCCATTTAAATGTGAGCGGAATTCAGTGTCTTCTGTC 302  
Qy 301 TGGCAGACGTGGAAGATCTTTATTCACAGCAGATTTTCCACGACACAGTCCAGCCCGAG 360  
Db 303 TGGCAGACGTGGAAGATCTTTATTCACAGCAGATTTTCCACGACACAGTCCAGCCCGAG 362  
Qy 361 CCTCCGATCGTACTGAACAGTATCACTCACTAAATGAATCTATTTCTGGATGAAT 420  
Db 363 CCTCCGATCGTACTGAACAGTATCACTCACTAAATGAATCTATTTCTGGATGAAT 422  
Qy 421 TTATACTGAGAGCATCTGTATATGTTTACAAATTCACATTTGGATTCCTCATTTGAGA 480  
Db 423 TTATACTGAGAGCATCTGTATATGTTTACAAATTCACATTTGGATTCCTCATTTGAGA 482  
Qy 481 AGTACCCACTCTATGTTTTTAA-----AGTTTTCTGGAAGAAACAACAG 525  
Db 483 AGTACCCACTCTATGTTTTTAAAGGTTTTCTTTGAGCAGGTTTTCTGGAAGAAACAACAG 542  
Qy 526 CCAAAAATGCGATATGATTTGACTGTGGAATTCATGCGAGAGTGGATCTCTCTGCTT 585  
Db 543 CCAAAAATGCGATATGATTTGACTGTGGAATTCATGCGAGAGTGGATCTCTCTGCTT 602  
Qy 586 TCTGCTTGGTTCATAGGCAAT----- 608  
Db 603 TCTGCTTGGTTCATAGGCAATATACTCAATTTCTATGGGATAATAGGGCAATATACCA 662  
Qy 609 ----- 608  
Db 663 ATCTCTGAGGCTTGTGGATTTCTATGTTATGCGAGTGGTTAATGTGGATGGTTATGACT 722  
Qy 609 -----AATCGAATGTGGAAGAAAGACCGTTCTTTCTATGCGAACAATCATTT 654  
Db 723 ACTCATGGAAGAAATCGAATGTGGAAGAAAGACCGTTCTTTCTATGCGAACAATCATTT 782

RESULT 5  
US-10-115-479-69  
; Sequence 69, Application US/10115479



Db 1154 ACGATTGGATCTATGATTTGGGCATCAAAATATTCGTTTACAAATTTGAACTTCGAGATACGG 1213  
Qy 1051 -----TTACATCAAAACCCACCTGTAGAGAAGCTTTTG 1082  
Db 1214 GCACATAGCGATCTTCTGCTGCCGAGGCTTACATCAAAACCCACCTGTAGAGAAGCTTTTG 1273  
Qy 1083 CCGCTGTCTCTAAATAGCTTGGCATGCTATTAGGAATTTTAAATGCCCTCGATTTTATC 1142  
Db 1274 CCGCTGTCTCTAAATAGCTTGGCATGCTATTAGGAATTTTAAATGCCCTCGATTTTATC 1333  
Qy 1143 ATTCTGCTTC 1152  
Db 1334 ATTCTGCTTC 1343

RESULT 6  
US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: TAFI  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

Query Match 54.68; Score 858.8; DB 15; Length 1272;  
Best Local Similarity 83.94; Pred. No. 3.1e-209; Mismatches 42; Indels 163; Gaps 2;  
Matches 1067; Conservative 0;

Qy 18 ATGAAGCTTTGCGAGCCTTGTCAGTCTTGTATCCCATTTCTTCTGTGTAGAGCATGTC 77  
Db 1 ATGAGCTTTGCGAGCTTGTAGTCTTGTATCCCATTTCTTCTGTGTAGAGCATGTC 60  
Qy 78 TTCGGTTCAGAGTGCGCCAAAGTTCTAGTCTTCTTCTAGAACCTCTAGGCAAGTTCAA 137  
Db 61 TTCGGTTCAGAGTGCGCCAGGTTCTAGTCTTCTTCTAGAACCTCTAGGCAAGTTCAA 120  
Qy 138 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGAGCGCGTTAAGCTGAC 197  
Db 121 GTGCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGAGCGCGTTAAGCTGAC 180  
Qy 198 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTGTAATGCATCTGATGTCGACAAATGTG 257  
Db 181 CTTATTGAGAGAAAAAACAAGTCCATTTTGTGTAATGCATCTGATGTCGACAAATGTG 240  
Qy 258 AAAGCCCATTTAAATGTAGCGGAATTTCCATGAGTGTCTTGTGGCAGACGTGGAAGAT 317  
Db 241 AAAGCCCATTTAAATGTAGCGGAATTTCCATGAGTGTCTTGTGGCAGACGTGGAAGAT 300  
Qy 318 CTTATTCAACAGCAGATTTTCCACGACACAGTACGCCCCCGAGCTCCGATCGTACTAT 377  
Db 301 CTTATTCAACAGCAGATTTTCCACGACACAGTACGCCCCCGAGCTCCGATCGTACTAT 360  
Qy 378 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGCAT 437  
Db 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGTAT 420  
Qy 438 CTTGATATGCTTACAAAAATCCCATTTGGATCTCTATTTGAGAGTACCCACTTATGTT 497  
|||||

Db 421 CTTGATATGCTTACAAAAATCCCATTTGGATCTCTCTATGAGAGCACCACCTTTATGTT 480  
Qy 498 TTAAGGTTTTCTGGAAGAAGCAAAACAGCCAAAATGCCATATGGATTGACTGTGGAATC 557  
Db 481 TTAAGGTTTTCTGGAAGAAGCAAAACAGCCAAAATGCCATATGGATTGACTGTGGAATC 540  
Qy 558 CATGCCAGAGAATGATCTCTCTCTGCTTTCTGCTGTGTTTCTATAGGCCAT----- 608  
Db 541 CATGCCAGAGAATGATCTCTCTCTGCTTTCTGCTGTGTTTCTATAGGCCATATAAATGAA 600  
Qy 609 ----- 608  
Db 601 TACTACGGGATATAGGGGAATATACCAATTTCTGAGGCATGTGGATTTCTATGTTATG 660  
Qy 609 -----AATCGAATGTGAGAAAG 626  
Db 661 CCACTGGTTAATGTGGATGTTATGACTACTCATGGAAGAAAGAAATCGAATGTGAGAAAG 720  
Qy 627 AACCGTTCTTTCTATCGGAACAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTC 686  
Db 721 AACCGTTCTTTCTATCGGAACAATCGTTGCATCGGAACAGACCTGAACAGCAACTTTGCG 780  
Qy 687 TCAAAACACTGTGTGAGGAAGTGATCCAGTTCTCATGCTCGGAACACTACTGTGGA 746  
Db 781 TCAAAACACTGTGTGAGGAAGTGATCCAGTTCTCATGCTCGGAACACTACTGTGGA 840  
Qy 747 CTTTATCTGAGTCAGAACCCAGAAAGTGAAGGAGTGTGCTAGTTCTTGTGAGAAGAAATATC 806  
Db 841 CTTTATCTGAGTCAGAACCCAGAAAGTGAAGGAGTGTGCTAGTTCTTGTGAGAAGAAATATC 900  
Qy 807 AACCAATTAAGCATATCATGATGCTATCTACTCCAGCATATAGTGTGTTTCCATAT 866  
Db 901 AACCAATTAAGCATATCATGATGCTATCTACTCCAGCATATCGTGTGTTTCCATAT 960  
Qy 867 TCCTATACAGAAATGAAGCAAGACCATGAGGAATCTGTCTCTAGTAGCCAGTGAAGCA 926  
Db 961 TCCTATACAGAAATGAAGCAAGACCATGAGGAATCTGTCTCTAGTAGCCAGTGAAGCA 1020  
Qy 927 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGATATACACATGCGCATGCTCAGAA 986  
Db 1021 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGATATACACATGCGCATGCTCAGAA 1080  
Qy 987 ACCTTATACCTAGTCTCTGAGGTGGGAGCGAATGGAATCTATGATTTGGSCATCAATAT 1046  
Db 1081 ACCTTATACCTAGTCTCTGAGGTGGGAGCGAATGGAATCTATGATTTGGSCATCAATAT 1140  
Qy 1047 TCGT-----TTAC 1054  
Db 1141 TCGTTTACAATTTGAATCTCGAGATACGGGCAAAATACGGATTTCTTGTGCTGAGCGTTAC 1200  
Qy 1055 ATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGTCATT 1114  
Db 1201 ATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGTCATT 1260  
Qy 1115 AGGAATGTTTAA 1126  
Db 1261 AGGAATGTTTAA 1272

RESULT 7  
US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12



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; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Query Match      54.3%; Score 853.8; DB 9; Length 1400;
Best Local Similarity 93.3%; Pred. No. 6.3e-208;
Matches 934; Conservative 1; Mismatches 13; Indels 53; Gaps 2;

Qy 607 ATAATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAACAAATCATTGTCATCGGAACAG 666
Db 177 AGAATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAACAAATCATTGTCATCGGAACAG 236

Qy 667 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCAT 726
Db 237 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCAT 296

Qy 727 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACAGAGTGAAGGCGAGTGGCTA 786
Db 297 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACAGAGTGAAGGCGAGTGGCTA 356

Qy 787 GTTTCCTTGAGAAAGAAATATCAACAGATTAAGCATACATCAGCATGCATTTCATCTCCC 846
Db 357 GTTTCCTTGAGAAAGAAATATCAACAGATTAAGCATACATCAGCATGCATTTCATCTCCC 416

Qy 847 AGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGT 906
Db 417 AGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGT 476

Qy 907 CTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAACCAAGGTATA 966
Db 477 CTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAACCAAGGTATA 536

Qy 967 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCT 1026
Db 537 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCT 596

Qy 1027 ATGATTTGGGCATCAATATTCGT----- 1050
Db 597 ATGATTTGGGCATCAATATTCGT----- 1050

Qy 1051 -----TTACATCAAAACCCACCTCTGAGAGAGCTTTTGGCGCTGTCTCTA 1094
Db 657 TCTTGCTGCCGGAGCGTTACATCAAAACCCACCTCTGAGAGAGCTTTTGGCGCTGTCTCTA 716

Qy 1095 AAATAGCTTGGCATGTCTATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCG 1154
Db 717 AAATAGCTTGGCATGTCTATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCG 776

Qy 1155 TATTTTAAATTTACTGATTCAGAGAACCAATATCTGATTCAGATTAATTTTAAAGTTT 1214
Db 777 TATTTTAAATTTACTGATTCAGAGAACCAATATCTGATTCAGATTAATTTTAAAGTTT 836

Qy 1215 ATCCGTAGTTTGTATAAAGATTTTCTTATTCCTTGGTTCGTGAGAGAACCTAATAAGT 1274
Db 837 ATCCGTAGTTTGTATAAAGATTTTCTTATTCCTTGGTTCGTGAGAGAACCTAATAAGT 896

Qy 1275 GCTACTTTGCAATTAAGGACAGTATGGTTCATGCTTTTATCCCTTTTAAATAAATAATG 1334
Db 897 GCTACTTTGCAATTAAGGACAGTATGGTTCATGCTTTTATCCCTTTTAAATAAATAATG 955

Qy 1335 TAAAGTCTAGTTACTTACTTTTCTTTGATTTTCGAGGTTTGACTAGCCATCTCAAGCA 1394
Db 956 TAAAGTCTAGTTACTTACTTTTCTTTGATTTTTCGAGGTTTGACTAGCCATCTCAAGCA 1015

Qy 1395 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCAGCGTGTAT 1454
Db 597 ATGATTTGGGCATCAATATTCGT----- 1050

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05913
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

RESULT 8
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05913
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Query Match      54.3%; Score 853.8; DB 10; Length 1400;
Best Local Similarity 93.3%; Pred. No. 6.3e-208;
Matches 934; Conservative 1; Mismatches 13; Indels 53; Gaps 2;

Qy 1016 ACTTTGACGTTTGACTAGCCATCTCAAACAAAGTAAATCAANGATCATCTCAGCGTGTAT 1075
Db 1455 CATTTGATCTCTACTCAACAAAGGAAGGTGTCAGAGTACATTAAGATTTCTGCTCC 1514
Db 1076 CATTTGATCTCTACTCAACAAAGGAAGGTGTCAGAGTACATTAAGATTTCTGCTCC 1135

Qy 1515 AAATTTTCATATAATTTCTTCTCTCTCTTAAATAAATAAATAA 1555
Db 1136 AAATTTTCATATAATTTCTGCTTGTGCTTTAGAAATACAA 1176

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05913
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Query Match      54.3%; Score 853.8; DB 10; Length 1400;
Best Local Similarity 93.3%; Pred. No. 6.3e-208;
Matches 934; Conservative 1; Mismatches 13; Indels 53; Gaps 2;

Qy 607 ATAATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAACAAATCATTGTCATCGGAACAG 666
Db 177 AGAATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAACAAATCATTGTCATCGGAACAG 236

Qy 667 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCAT 726
Db 237 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCAT 296

Qy 727 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACAGAGTGAAGGCGAGTGGCTA 786
Db 297 GCTCGGAACCTACTGTGGACTTTATCCTGAGTCAGAACAGAGTGAAGGCGAGTGGCTA 356

Qy 787 GTTTCCTTGAGAAAGAAATATCAACAGATTAAGCATACATCAGCATGCATTTCATCTCCC 846
Db 357 GTTTCCTTGAGAAAGAAATATCAACAGATTAAGCATACATCAGCATGCATTTCATCTCCC 416

Qy 847 AGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGT 906
Db 417 AGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGT 476

Qy 907 CTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAACCAAGGTATA 966
Db 477 CTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAACCAAGGTATA 536

Qy 967 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCT 1026
Db 537 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGAGCATTTGGATCT 596

Qy 1027 ATGATTTGGGCATCAATATTCGT----- 1050
Db 597 ATGATTTGGGCATCAATATTCGT----- 1050

Qy 1051 -----TTACATCAAAACCCACCTCTGAGAGAGCTTTTGGCGCTGTCTCTA 1094
Db 657 TCTTGCTGCCGGAGCGTTACATCAAAACCCACCTCTGAGAGAGCTTTTGGCGCTGTCTCTA 716

Qy 1095 AAATAGCTTGGCATGTCTATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCG 1154
Db 717 AAATAGCTTGGCATGTCTATTAGGAATGTTTAATGCCCTGATTTTATCATTTCTGCTTCCG 776

Qy 1155 TATTTTAAATTTACTGATTCAGAGAACCAATATCTGATTCAGATTAATTTTAAAGTTT 1214
Db 777 TATTTTAAATTTACTGATTCAGAGAACCAATATCTGATTCAGATTAATTTTAAAGTTT 836

Qy 1215 ATCCGTAGTTTGTATAAAGATTTTCTTATTCCTTGGTTCGTGAGAGAACCTAATAAGT 1274
Db 837 ATCCGTAGTTTGTATAAAGATTTTCTTATTCCTTGGTTCGTGAGAGAACCTAATAAGT 896

Qy 1275 GCTACTTTGCAATTAAGGACAGTATGGTTCATGCTTTTATCCCTTTTAAATAAATAATG 1334
Db 897 GCTACTTTGCAATTAAGGACAGTATGGTTCATGCTTTTATCCCTTTTAAATAAATAATG 955

Qy 1335 TAAAGTCTAGTTACTTACTTTTCTTTGATTTTCGAGGTTTGACTAGCCATCTCAAGCA 1394
Db 956 TAAAGTCTAGTTACTTACTTTTCTTTGATTTTTCGAGGTTTGACTAGCCATCTCAAGCA 1015

Qy 1395 ACTTTCGACGTTTGACTAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCAGCGTGTAT 1454
Db 597 ATGATTTGGGCATCAATATTCGT----- 1050
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Qy	1051	-----TTACATCAAA	CCCACTCTAGAGAAGCTTTTGC	CGCTGTCTCTA	1094
Db	657	TC	TGCTGCOGAGCGTTACATCAAA	CCCACTCTAGAGAAGCTTTTGC	CGCTGTCTCTA 716
Qy	1095	AAATAGCTTGGCATGT	CATTAGGAATGTTTAATCC	CCCTGANTTTATCATTTCTGCTTCCG	1154
Db	717	AAATAGCTTGGCATGT	CATTAGGAATGTTTAATCC	CCCTGANTTTATCATTTCTGCTTCCG	776
Qy	1155	TATTTTAA	TTTATCTGATCCAGCAAGACCA	AAATCATTTGTATCAGATATTTTTTAAGTTTT	1214
Db	777	TATTTTAA	TTTATCTGATCCAGCAAGACCA	AAATCATTTGTATCAGATATTTTTTAAGTTTT	836
Qy	1215	ATCCGTAGTTTTGATAA	AGANTTTTCTATCTCTTTTAC	CCCTTTAAAAAAAATTG	1334
Db	837	ATCCGTAGTTTTGATAA	AGANTTTTCTATCTCTTTTAC	CCCTTTAAAAAAAATTG	896
Qy	1275	GCTACTTTGGCATTAA	GGCAGACTAGGGTTCATCTCTTTTAC	CCCTTTAAAAAAAATTG	1334
Db	897	GCTACTTTGGCATTAA	GGCAGACTAGGGTTCATCTCTTTTAC	CCCTTTAAAAAAAATTG	955
Qy	1335	TAAAGTCTAGTTAC	TACTTTTTTCTTTGATTTTCGACGTTGAC	TAGCCATCTCAAGCA	1394
Db	956	TAAAGTCTAGTTAC	TACTTTTTTCTTTGATTTTCGACGTTGAC	TAGCCATCTCAAGCA	1015
Qy	1395	ACTTTTCACGTTTGAC	TAGCCATCTCAAGCAAGTTTAATCA	AAGATCATCTCAGCTGAT	1454
Db	1016	ACTTTTCACGTTTGAC	TAGCCATCTCAAGCAAGTTTAATCA	AAGATCATCTCAGCTGAT	1075
Qy	1455	CATTGGATCCTACTCA	ACAAAAGGAGGGTGCAGAA	GTACATTAAGATTTCTGCTCC	1514
Db	1076	CATTGGATCCTACTCA	ACAAAAGGAGGGTGCAGAA	GTACATTAAGATTTCTGCTCC	1135
Qy	1515	AAATTTTCA	TAAATTTCTTCTCTCTTTAAAA	AAAAAAA	1555
Db	1136	AAATTTTCA	TAAATTTCTGCTGTGACCTTAGAA	ATACAA	1176

## RESULT 9

US-10-115-479-63

Sequence 63, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479

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; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63

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Query Match	43.7%	Score 688;	DB 16;	Length 1037;
Best Local Similarity	79.3%;	Pred. No. 1.6e-165;		
Matches 955;	Conservative 0;	Mismatches 5;	Indels 244;	Gaps 2;
Qy	1	AGAAAAATGCTGTTGGGATCGAAGCTTTGCAGCCCTTCAGTGGCCAAAGTTCTAGTCGTCTTCTCTCT	60	
Db	24	AGAAATGCTGTTGGATGAGCTTTGCAGCTTTCGAGTCTTGCAGTCTTGTACCAATGTTCTCT	83	
Qy	61	TCTGTGAGCAGCATGCTTCGCGTTCCAGAGTGGCCAAAGTTCTAGTCGTCTTCTCTCTAGAA	120	
Db	84	TCTGTGAGCAGCATGCTTCGCGTTTCAGAGTGGCCAAAGTTCTAGTCGTCTTCTCTCTAGAA	143	
Qy	121	CCTCTAGGCAAGTTCAGTTCCTACAGAACTCTTACTACAACATATGAGATGTTCTCTCTGGC	180	
Db	144	CCTCTAGGCAAGTTCAGTTCCTACAGAACTTACTACAACATATGAGATGTTCTCTCTGGC	203	
Qy	181	AGCCGGTAAACAGCTGACCTTTATTGTGAAGAAAAAACAAGTCCATTTTTTGTAAATGTCAT	240	
Db	204	AGCCGGTAAACAGCTGACCTTTATTGTGAAGAAAAAACAAGTCCATTTTTTGTAAATGTCAT	263	
Qy	241	CTGATGTGCAAAATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGC	300	
Db	264	CTGATGTGCAAAATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGC	323	
Qy	301	TGCGACAGCTGGGAAGATCTTTATTCACACGACAGATTTCCACGACACAGTCAGCCCCCGAG	360	
Db	324	TGGCAGCAGTGGGAAGATCTTTATTCACACGACAGATTTCCACGACACAGTCAGCCCCCGAG	383	
Qy	361	CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAAT	420	
Db	384	CCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAAT	443	
Qy	421	TTATACTGAGAGGCATCTGATATGCTTACAAAAATCCACATTGGAATCCTCATTTTGAGA	480	
Db	444	TTATACTGAGAGGCATCTGATATGCTTACAAAAATCCACATCCGATCCTCATTTTGAGA	503	
Qy	481	AGTACCACCTCTATGTTTAAAGGTTTCTGGAAAAAGAACAAACAGGCAAAAAATGCCATAT	540	
Db	504	AGTACCACCTCTATGTTTAAAGGTTTCTGGAAAAAGAACAAACAGGCAAAAAATGCCATAT	563	
Qy	541	GGATTGACTGTGGAATCCCATGCCAGAGAAATGGATCTCTCTCTGCTTTCTGCTGTGGTTCA	600	

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Db 564 GATTG----- 569
Qy 601 TAGCCATAATCGAATGTGGAGAAAGAACCGTCTTCTTATGCGAACAAATCATTTGCATCG 660
Db 570 ----- 569
Qy 661 GAACAGACCTGAATAGCAACTTTGTCTCCAAACNACTGGTGTGAGGAAGGTGCATCCAGTT 720
Db 570 ----- 569
Qy 721 CCTCATGCTCGAAACCTACTGTGCACTTTATCTGAGTCAGAACACAGAAAGTGAAGSCAG 780
Db 570 -----ACTGTGACTTTATCTGAGTCAGAACACAGAAAGTGAAGSCAG 611
Qy 781 TGGCTAGTTCTTGTAGAGAAATATCAACAGATTTAAAGCATACATCAGCATGCAATTCAT 840
Db 612 TGGCTAGTTCTTGTAGAGAAATATCAACAGATTTAAAGCATACATCAGCATGCAATTCAT 671
Qy 841 ACTCCAGCATATAGTGTCTCCATATTTCTATACACAGAGTAAAGCAAGACCATGAGG 900
Db 672 ACTCCAGCATATAGTGTCTCCATATTTCTATACACAGAGTAAAGCAAGACCATGAGG 731
Qy 901 AACTGTCTCTAGTAGGACAGTGAAGCAGTTCGTCTATTGACAAAATAGTAAAAATACCA 960
Db 732 AACTGTCTCTAGTAGGACAGTGAAGCAGTTCGTCTATTGAGAAAATAGTAAAAATACCA 791
Qy 961 GGTATACACATGGCCATGGCTCAGAAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATT 1020
Db 792 GGTATACACATGGCCATGGCTCAGAAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATT 851
Qy 1021 GGATCTATGATTTGGGCATCAATATTTGGT----- 1050
Db 852 GGAFTCTATGATTTGGGCATCAAAATATTCGTTTACAATTGAACTTCGAGATACGGGCACAT 911
Qy 1051 -----TTACATCAAAACCCACTGTAGAGAAAGCTTTTGGCCGCTG 1088
Db 912 ACGAATCTTGCTGCCGGAGGTTACATCAAACCCACTGTAGAGAAAGCTTTTGGCCGCTG 971
Qy 1089 TCTCTAAATAGCTTGGCATGTCTAATAGGAATGTTTAAATGCCCTGATTTATCAATCTG 1148
Db 972 TCTCTAAATAGCTTGGCATGTCTAATAGGAATGTTTAAATGCCCTGATTTATCAATCTG 1031
Qy 1149 CTTC 1152
Db 1032 CTTC 1035
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## RESULT 10

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US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
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; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65
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Query Match 38.8%; Score 610.4; DB 16; Length 1132;
Best Local Similarity 85.2%; Pred. No. 1.3e-145;
Matches 760; Conservative 0; Mismatches 6; Indels 126; Gaps 2;
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Qy 1 AGAAAATTGCTGTGGGATGAAGCTTTGACGCTTGACGTCCTTGACCAATGTTCTCT 60
Db 24 AGAAAATTGCTGTGGGATGAAGCTTTGACGCTTGACGTCCTTGACCAATGTTCTCT 83
Qy 61 TCTGTGAGCAGCATGTCTTCGGCTTCAGAGTGGCCCAAGTTCTAGCTGCTCTTCTAGAA 120
Db 84 TCTGTGAGCAGCATGTCTTCGGCTTCAGAGTGGCCCAAGTTCTAGCTGCTCTTCTAGAA 143
Qy 121 CCTCTAGGCAAGTTCAGGTTCTACAGAACTTACTACAAACATATGAGATGTTCTCTGGC 180
Db 144 CCTCTAGGCAAGTTCAGGTTCTACAGAACTTACTACAAACATATGAGATGTTCTCTGGC 203
Qy 181 AGCCGGTAAACAGCTGACCTTTATTTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCAT 240
Db 204 AGCCGGTAAACAGCTGACCTTTATTTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCAT 263
Qy 241 CTGATGTGCAATGTGAAGCCCATTTTAAATGTGAGCGGAATTCATGAGTGTCTTTC 300
Db 264 CTGATGTGCAATGTGAAGCCCATTTTAAATGTGAGCGGAATTCATGAGTGTCTTTC 323
Qy 301 TGGCAGACGTGGAAGATCTTTATTTCAACACAGATTTTCCAAACGACACAGTCAAGCCCCGAG 360
Db 324 TGGCAGACGTGGAAGATCTTTATTTCAACACAGATTTTCCAAACGACACAGTCAAGCCCCGAG 383
Qy 361 CCTCCGCATCGTACTATGAACAGTATCACCTCACTAAATGAAATCTATTTCTTGGATAGAT 420
Db 384 CCTCCGCATCGTACTATGAACAGTATCACCTCACTAAATGAAATCTATTTCTTGGATAGAT 443
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QY 421 TTATAACTGAGGACCTCTGATATGCTTACAAAAATCCACATTCATCTCTATTTGAGA 480
DB 444 TTATAACTGAGGACCTCTGATATGCTTACAAAAATCCACATTCATCTCTATTTGAGA 503
QY 481 AGTACCCACCTCTATGTTTTAA-----AGGTTTCTGGAAAAAGAACAG 525
DB 504 AGTACCCACCTCTATGTTTTAAAGGGTTTCTTTGAGCAGGTTTCTGGAAAAAGAACAG 563
QY 526 CCAAAATGCCATATGATGACTGTGGAATCCATGCCAGAGATGATCTCTCTGCTT 585
DB 564 CCAAAATGCCATATGATGACTGTGGAATCCATGCCAGAGATGATCTCTCTGCTT 623
QY 586 TCTGCTTGTGTTTCATAGGCCAT----- 608
DB 624 TCTGCTTGTGTTTCATAGGCCATATACTCAATCTATGGGTAATAGGGCAATATACCA 683
QY 609 ----- 608
DB 684 ATCTCTGAGGCTTGTGGAATTTCTATGTTATGCGGTGTTAATGTGGATGTTATGACT 743
QY 609 -----AATCGAATGGAGAAAGAACCGTTCTTCTATGCGAACAATCAT 654
DB 744 ACTCATGGAATAAGATCGAATGGAGAAAGAACCGTTCTTCTATGCGAACAATCAT 803
QY 655 GCATCGGAACAGACCTCAATAGCAACTTTGTCTCCAAACACTGTGTGAGGAAGGTGCAT 714
DB 804 GCATCGGAACAGACCTCAATAGCAACTTTGTCTCCAAACACTGTGTGAGGAAGGTGCAT 863
QY 715 CCAATTCCTCATGCTCGGAACCTACTGTGACATTTATCTGAGTCAGAAC 766
DB 864 CCAATTCCTCATGCTCGGAACCTACTGTGACATTTATCTGAGTCAGAAC 915

RESULT 11
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 30.4%; Score 478.6; DB 9; Length 55827;
Best Local Similarity 98.0%; Pred. No. 5.8e-111;
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1051 TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGT 1110
DB 53334 TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGT 53393
QY 1111 CATTAGGAATGTTTAATGCCCTGATTTATCATCTTCGCTTCGATTTTAATTTACTGA 1170
DB 53394 CATTAGGAATGTTTAATGCCCTGATTTATCATCTTCGCTTCGATTTTAATTTACTGA 53453
QY 1171 TTCCAGAACACCAATCATTTATCATCTTCGCTTCGATTTTAATTTACTGA 1230
DB 53454 TTCCAGAACACCAATCATTTATCATCTTCGCTTCGATTTTAATTTACTGA 53513
QY 1231 AAAGATTTCTATTCCTGTTTCTGTCAGAGAACCTTAATAGTGTACTTTGCCATTAA 1290
DB 53514 AAAGATTTCTATTCCTGTTTCTGTCAGAGAACCTTAATAGTGTACTTTGCCATTAA 53573
QY 1291 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 1350
DB 53574 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 53632
QY 1351 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 1410
DB 53633 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 53692
QY 1411 TAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCATTTGGATCCTACTCA 1470
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QY 1291 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 1350
DB 53574 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 53632
QY 1351 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 1410
DB 53633 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 53692
QY 1411 TAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCATTTGGATCCTACTCA 1470
DB 53693 TAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCATTTGGATCCTACTCA 53752
QY 1471 AAAAAAGGAGGGTGTGTCAGAGTACATTAAGAGATTTCTGCTCCAAATTTTCAATAAAT 1530
DB 53753 AAAAAAGGAGGGTGTGTCAGAGTACATTAAGAGATTTCTGCTCCAAATTTTCAATAAAT 53812
QY 1531 TCTTCTTCTCTTTTAAAAAATAAAAA 1555
DB 53813 TCTGCTTGTGCTTTTAGAATAACAA 53837

RESULT 12
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US2003001757A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Query Match 30.4%; Score 478.6; DB 14; Length 55827;
Best Local Similarity 98.0%; Pred. No. 5.8e-111;
Matches 495; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1051 TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGT 1110
DB 53334 TTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTAAATAGCTTGGCATGT 53393
QY 1111 CATTAGGAATGTTTAATGCCCTGATTTATCATCTTCGCTTCGATTTTAATTTACTGA 1170
DB 53394 CATTAGGAATGTTTAATGCCCTGATTTATCATCTTCGCTTCGATTTTAATTTACTGA 53453
QY 1171 TTCCAGAACACCAATCATTTATCATCTTCGCTTCGATTTTAATTTACTGA 1230
DB 53454 TTCCAGAACACCAATCATTTATCATCTTCGCTTCGATTTTAATTTACTGA 53513
QY 1231 AAAGATTTCTATTCCTGTTTCTGTCAGAGAACCTTAATAGTGTACTTTGCCATTAA 1290
DB 53514 AAAGATTTCTATTCCTGTTTCTGTCAGAGAACCTTAATAGTGTACTTTGCCATTAA 53573
QY 1291 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 1350
DB 53574 GGAGACTAGGGTTCATGCTTTTACCCTTTAAAAAATTTGTAAGTCTAGTTACC 53632
QY 1351 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 1410
DB 53633 TACTTTTCTTTGATTTTTCGAGTTCATCTCAAGCACTCTTTCGAGCTTTGAC 53692
QY 1411 TAGCCATCTCAAGCAAGTTTAAATCAAGATCATCTCACGCTGATCATTTGGATCCTACTCA 1470
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Db 53693 TAGCACTCAGCAAGTTTAAATCAATGATCACTCAGCTGATCGATCGATCTACTCA 53752
Qy 1471 ACAAAGGAAGGGTGTGAGAGTACATTAAGAGTTTCTGCTCCAAATTTTCAATAAATT 1530
Db 53753 ACAAAGGAAGGGTGTGAGAGTACATTAAGAGTTTCTGCTCCAAATTTTCAATAAATT 53812
Qy 1531 TCTTCTTCTCTTTTAAAAAAA 1555
Db 53813 TCTGCTTGTGCTTTAGAAATACAA 53837

RESULT 13
US-09-960-352-14595
; Sequence 14595, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14595
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 62-LIB34-032-Q1-E1-H10
US-09-960-352-14595

Query Match 21.1%; Score 331.2; DB 9; Length 416;
Best Local Similarity 87.3%; Pred. No. 2.5e-74;
Matches 363; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 167 GATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATTGTGAAGAAAAACAAGTCCATTT 226
Db 1 GATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATTGTGAAGAAAAACAAGTCCATTT 60
Qy 227 TTTTGTAAATGCATCTGATGTGCAATGTGAAAGCCCATTTAAATGTGAGCGGAATTC 286
Db 61 TTTTGTGAATGCATCTGATGTGAAAGTGTGAAAGCCCATTTAAATGTGAGCGGAATTC 120
Qy 287 ATGCAGTGTCTTGTGCGCAGCGTGGAGATCTTTATTCAACAGCAGATTTCCAAACGAC 346
Db 121 ATTCAGGGTCTGGTGGAAAAATGTGGAAGATCTTTATCCGGCAGCAGACTTCCAATGAC 180
Qy 347 AGTCAGCCCCCGACCTCCGATCGTACTATGACAGTATCACTCACTAATGAAATCTA 406
Db 181 CATCAGCCCCCGGCATCTCTCTACTATGAAACAGTATCACTCACTAATGAGATCTA 240
Qy 407 TTCTTGGATAGAAATTAATCACTGAGCGCATCTTGATATGTTTACAAAAATCCACATTGG 466
Db 241 TTCTTGGATAGAAATTAATCACTGAGCGGTATCTTGATATGTTTGA AAAATCCACATTGG 300
Qy 467 ATCTCTATTTGAGAGTACCCACTCTATGTTTAAAGGTTTCTGGA AAAAGAACAAACAGC 526
Db 301 ATCTCTATCAGAGAATACCCACTTTATGTTTAAAGGTTTCTTAAAAAGAACAAAGGCG 360
Qy 527 CAAAAATGCCATATGGAATGATCTGTGGAATCCATGCCAGAGATGGATCTCTCTG 582
Db 361 CAAAAATGCCATATGGAATGATCTGTGGAATCCATGCCAGAGAGTGGATCTCTCTG 416

RESULT 14
US-09-960-352-8425
; Sequence 8425, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
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; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8425
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB34-005-Q1-E1-A12
US-09-960-352-8425

Query Match 18.2%; Score 286.8; DB 9; Length 397;
Best Local Similarity 83.9%; Pred. No. 5.8e-63;
Matches 324; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 12 GTTGGGATGAAGCTTTTCAGCCTTTCAGTCTTGTACCCATTTCTTCTCTCTGAGCAG 71
Db 12 GTGGGATGAAGCTTTTATAGCTTTGGGAGTCTTGTCCACCCTGCTTCTTCTGTTGGGAG 71
Qy 72 CATGCTTTCGCGTTCAGAGTGGCCAAGTCTAGCTGCTCTTCTAGAACTCTTAGGCAA 131
Db 72 CATGCTTTCGCTTTCAGAGGGGCCAGGTTTTATCTGCTTCTCTAGAACTCTCAGGCAA 131
Qy 132 GTTCAAGTTCTACAGAACTTTACTACAATATGAGATTTCTTCTGGCAGCGGTAA 191
Db 132 GTTCAAAATCTGCAGAAATTTACTACAATATGAGATTTCTTCTGGCAGCGGTAA 191
Qy 192 GCTGACCTTATGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCAC 251
Db 192 GCTGAATATATGTGAAGGATACGAAGTCCATTTTGTGAATGCATCTGATGTAAGC 251
Qy 252 AATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGCAAGTCTTCTGTCGAGACGTG 311
Db 252 AATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGCAAGTCTTCTGTCGAGACGTG 311
Qy 312 GAAGATCTTATTCAGCAGAGATTTCCACGACAGTTCAGCCCCCGAGGCTCCGATCG 371
Db 312 GAAGATCTTATCCGGCAGCAGACTTCCAAATGACACCATCAGCCCCCGGATCTCTCTCC 371
Qy 372 TACTATGACAGTATCACTCACTAAA 397
Db 372 TACTATGACAGTATCACTCACTAAA 397

RESULT 15
US-09-917-800A-468/C
; Sequence 468, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917.800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
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; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/295,798  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/297,457  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,884  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,459  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 1740  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 468  
; LENGTH: 431  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA998857  
; NAME/KEY: misc feature  
; LOCATION: (1)..(431)  
; OTHER INFORMATION: n = a or c or g or t  
US-09-917-800A-468

Query Match 8.7%; Score 137.2; DB 9; Length 431;  
Best Local Similarity 67.5%; Pred. No. 1.3e-24;  
Matches 268; Conservative 0; Mismatches 69; Indels 60; Gaps 3;  
  
Qy 894 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAACCTAGTAAA 953  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 431 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGACAAACCTAGTAAA 372  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 954 AATACCAAGGTATACACATGCGCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGG 1013  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 371 AACACCAAGGTATACACATGCGCATGGCTCAGAAAGTTTATATCTAGCTCCTGGAGGTCT 312  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 1014 GACGATTGGATCTATGATTTTGGCATCAAAATATTCGTTTA----- 1053  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 311 GATGATTGGATCTATGATTTTGGCATCAAAATATTCGTTTACGATTGAACCTTCGGGATACA 252  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 1054 -----CATCAAAACCCACCTCTAGAGAAGCTTTT 1081  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 251 GGCAGATACGGGTTCTTGGCTGCGTAGAGATTATCAAAACCCACTTCGCGAGAAGCTTTG 192  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 1082 GCGGCTGCTCTAAATAGCTTGGCATGTCTATTAGGAATGTTTAAATGCCCTCGATTTTAT 1141  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 191 GCGGCTGCTCTAAATAGCTTGGCATGTCTATCAGGAACAGTTAACACCC-----TTTC 138  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 1142 CATTCGCTTCGGTATTTTAAATTTACTGATTCAGCAAGACCAAAATCAATTGTATCAGAT- 1200  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 137 CTCTGCTCTCATTTACTTTTATTTTATTTGATTTTCTAGCAACACTAAATTTGTCACACTAGCTT 78  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 1201 -TATTTTAAAGTTTATCCGCTAGTTTGTATAAAGAT 1236  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 77 CTAGATTAAATCAGTTTCTTGGTTTGTGGAAGAT 41  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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OM protein - protein search, using sw model

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869.503 Million cell updates/sec

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Sequence: 1 MKLCSLAVLPVILFCEQHV.....IKYSFTSNPPVEXLLPLSLK 360

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1799.5	94.2	423	1	US-07-649-591B-3
3	1799.5	94.2	423	1	US-08-277-540-3
4	1799.5	94.2	423	1	US-08-430-787A-3
5	1799.5	94.2	423	2	US-08-869-057-2
6	1788.5	93.6	423	4	US-09-813-133A-4
7	640.5	33.5	404	1	US-08-696-139-2
8	639	33.4	415	2	US-08-860-882A-57
9	631.5	33.0	424	4	US-09-011-769A-39
10	628.5	32.9	417	1	US-09-011-769A-56
11	628.5	32.9	417	1	US-07-649-591B-7
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13	628.5	32.9	417	1	US-08-430-787A-7
14	623	32.6	716	3	US-09-171-945-125
15	619.5	32.4	417	1	US-07-649-591B-6
16	619.5	32.4	417	1	US-08-277-540-6
17	619.5	32.4	417	1	US-08-430-787A-6
18	619.5	32.4	417	4	US-09-917-254-66
19	604	31.6	307	2	US-08-782-760-6
20	604	31.6	307	5	PCT-US96-00995-6
21	604	31.6	437	4	US-09-675-305-10
22	604	31.6	437	4	US-10-200-344-10
23	603.5	31.6	396	1	US-07-649-591B-4
24	603.5	31.6	396	1	US-08-277-540-4
25	603.5	31.6	396	1	US-08-430-787A-4
26	576	30.1	306	1	US-08-696-139-4
27	561	29.4	329	4	US-09-011-769A-51

28	561	29.4	349	4	US-09-011-769A-47	Sequence 47, Appl
29	554	29.0	349	4	US-09-011-769A-60	Sequence 60, Appl
30	553	28.9	349	4	US-09-011-769A-64	Sequence 64, Appl
31	553	28.9	417	1	US-07-649-591B-8	Sequence 8, Appl
32	553	28.9	417	1	US-08-277-540-8	Sequence 8, Appl
33	553	28.9	417	1	US-08-430-787A-8	Sequence 8, Appl
34	546	28.6	399	4	US-09-710-099-8	Sequence 8, Appl
35	546	28.6	399	4	US-10-200-910-8	Sequence 8, Appl
36	543	28.4	613	3	US-09-171-945-113	Sequence 113, App
37	528.5	27.7	350	4	US-09-675-305-12	Sequence 12, Appl
38	528.5	27.7	350	4	US-10-200-344-12	Sequence 12, Appl
39	528.5	27.7	419	1	US-07-649-591B-5	Sequence 5, Appl
40	528.5	27.7	419	1	US-08-277-540-5	Sequence 5, Appl
41	528.5	27.7	419	1	US-08-430-787A-5	Sequence 5, Appl
42	519.5	27.2	436	4	US-09-710-099-6	Sequence 6, Appl
43	519.5	27.2	436	4	US-10-200-910-6	Sequence 6, Appl
44	513	26.8	417	3	US-08-640-906-4	Sequence 4, Appl
45	513	26.8	417	3	US-09-395-936-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinliu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: US\$ THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-813-133A-2

Query Match	95.1%	Score 1817;	DB 4;	Length 386;
Best Local Similarity	98.6%	Pred. No. 4.9e-189;	Mismatches 4;	Indels 0;
Matches 341;	Conservative 1;			Gaps 0;
Qy	1	MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTTEIVLWQPVTAD	60	
Db	1	MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTTEIVLWQPVTAD	60	
Qy	61	LIVKKQVHFFVNASDVNVKAHLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASY	120	
Db	61	LIVKKQVHFFVNASDVNVKAHLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASY	120	
Qy	121	EQVHSLNEIYSWTEFTTERHPDMLTKIHIGSSPEKPLVYLKVSKEQTAKNAIWDGCI	180	
Db	121	EQVHSLNEIYSWTEFTTERHPDMLTKIHIGSSPEKPLVYLKVSKEQTAKNAIWDGCI	180	
Qy	181	HAREWISPAFLWFIIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCERGSSSCSET	240	
Db	181	HAREWISPAFLWFIIGHNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCERGSSSCSET	240	
Qy	241	YCGLYPESPEVKAVASFLRRINQIKAYISMHSYSQHVFPYSTRSKSKDHEELSLVA	300	
Db	241	YCGLYPESPEVKAVASFLRRINQIKAYISMHSYSQHVFPYSTRSKSKDHEELSLVA	300	
Qy	301	SEAVRAIDKTSKNTRYTHGSGSETLVLPGGGDDWIYDLGIKYSFT	346	
Db	301	SEAVRAIEKISKNTRYTHGSGSETLVLPGGGDDWIYDLGIKYSFT	346	

RESULT 2

US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; US-07-649-591B-3

Query Match 94.2%; Score 1799.5; DB 1; Length 423;  
Best Local Similarity 89.6%; Pred. No. 4.6e-187;  
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;  
  
Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTD 60  
Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTD 60  
  
Qy 61 LIVKKQVHFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
  
Qy 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLVLYKVGKEQTAKNAIWDGCI 180  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLVLYKVGKEQTAKNAIWDGCI 180  
  
Qy 181 HAREWISPAFLWFIH-----NRMRK 203  
Db 181 HAREWISPAFLWFIHITQFYGIIGQYTNLLRLVDVFMVNVVDGYDYSWKKNRMRK 240  
  
Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSCSETYCGLYPSEPEVKAVASFLRNI 263  
Db 241 NRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPSEPEVKAVASFLRNI 300  
  
Qy 264 NQKAYISMSYSOHIVPPPYSTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHSE 323  
Db 301 NQKAYISMSYSOHIVPPPYSTRSKSDHEELSLVASEAVRALEKTSKNTRYTHGHSE 360  
  
Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGDDWIYDLGIKYSFT 383

RESULT 3  
US-08-277-540-3  
; Sequence 3, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1CID1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-277-540-3

Query Match 94.2%; Score 1799.5; DB 1; Length 423;  
Best Local Similarity 89.6%; Pred. No. 4.6e-187;  
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;  
  
Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTD 60  
Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTD 60  
  
Qy 61 LIVKKQVHFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120  
  
Qy 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLVLYKVGKEQTAKNAIWDGCI 180  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLVLYKVGKEQTAKNAIWDGCI 180  
  
Qy 181 HAREWISPAFLWFIH-----NRMRK 203  
Db 181 HAREWISPAFLWFIHITQFYGIIGQYTNLLRLVDVFMVNVVDGYDYSWKKNRMRK 240  
  
Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSCSETYCGLYPSEPEVKAVASFLRNI 263  
Db 241 NRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPSEPEVKAVASFLRNI 300



Qy 264 NQIKAYISMHSYSHQHVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 301 NQIKAYISMHSYSHQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360  
Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGDDWIYDLGIKYSFT 383

## RESULT 4

US-08-430-787A-3  
; Sequence 3, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Baton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-430-787A-3

Query Match 94.2%; Score 1799.5; DB 1; Length 423;  
Best Local Similarity 89.6%; Pred. No. 4.6e-187;  
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;  
Qy 1 MKCLSLAVLPVLPVLCFQHQVFAPQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60  
Db 1 MKCLSLAVLPVLPVLCFQHQVFAPQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60  
Qy 61 LIVKKQVHFVNASVDVNVKAHNVSGIPCSVLLADVEDLIQQOISNDTVSPRASYY 120  
Db 61 LIVKKQVHFVNASVDVNVKAHNVSGIPCSVLLADVEDLIQQOISNDTVSPRASYY 120  
Qy 121 EQYHSLNEIYSWTEFITERHPDMLTKIHIGSSPEKPYLYVLKVSQKEQTAKNAIWDICGI 180

Db 121 EQYHSLNEIYSWTEFITERHPDMLTKIHIGSSPEKPYLYVLKVSQKEQTAKNAIWDICGI 180  
Qy 181 HAREWISPAFCLWFIGH-----NRMRK 203  
Db 181 HAREWISPAFCLWFIGHITQFYGIICQYTNLLLVDFYVMPVNVVDGYDYSWKKNRMRK 240  
Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCBEAGASSSCSETYCGLYPESPEVKAVASFLRRNI 263  
Db 241 NRSFYANNHCIGTDLNRFASKHWCBEAGASSSCSETYCGLYPESPEVKAVASFLRRNI 300  
Qy 264 NQIKAYISMHSYSHQHVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 301 NQIKAYISMHSYSHQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSE 360  
Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGDDWIYDLGIKYSFT 383

## RESULT 5

US-08-869-057-2  
; Sequence 2, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Plasma  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 23..401  
US-08-869-057-2

Query Match 94.2%; Score 1799.5; DB 2; Length 423;  
Best Local Similarity 89.6%; Pred. No. 4.6e-187;  
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;  
Qy 1 MKCLSLAVLPVLPVLCFQHQVFAPQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60  
Db 1 MKCLSLAVLPVLPVLCFQHQVFAPQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60

Qy 61 LIVKKQVHFVNASVDNVKHAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120  
Db 61 LIVKKQVHFVNASVDNVKHAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120  
Qy 121 EQHSLNEIYSWIEFITERHDPDLTKIHGSSPEKPYLYVLKVSQKQTAKNAIWIDCGI 180  
Db 121 EQHSLNEIYSWIEFITERHDPDLTKIHGSSPEKPYLYVLKVSQKQTAKNAIWIDCGI 180  
Qy 181 HAREWISPAFLMFIH-----NRMRK 203  
Db 181 HAREWISPAFLMFIH-----NRMRK 203  
Qy 204 NRSFYANNHCIGTDLNNSFKWCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 241 NRSFYANNHCIGTDLNNSFKWCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 300  
Qy 264 NQIKAYISMHSYSHIYVFPYSYTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHSE 323  
Db 301 NQIKAYISMHSYSHIYVFPYSYTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHSE 360  
Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGDDWIYDLGIKYSFT 383  
RESULT 6  
US-09-813-133A-4  
; Sequence 4, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-813-133A-4  
Query Match 93.6%; Score 1788.5; DB 4; Length 423;  
Best Local Similarity 89.0%; Pred. No. 7.2e-186;  
Matches 341; Conservative 1; Mismatches 4; Indels 37; Gaps 1;  
Qy 1 MKLCSLAVLPVILVFCQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLMQPVTD 60  
Db 1 MKLCSLAVLPVILVFCQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLMQPVTD 60  
Qy 61 LIVKKQVHFVNASVDNVKHAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120  
Db 61 LIVKKQVHFVNASVDNVKHAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120  
Qy 121 EQHSLNEIYSWIEFITERHDPDLTKIHGSSPEKPYLYVLKVSQKQTAKNAIWIDCGI 180  
Db 121 EQHSLNEIYSWIEFITERHDPDLTKIHGSSPEKPYLYVLKVSQKQTAKNAIWIDCGI 180  
Qy 181 HAREWISPAFLMFIH-----NRMRK 203  
Db 181 HAREWISPAFLMFIH-----NRMRK 203  
Qy 204 NRSFYANNHCIGTDLNNSFKWCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 241 NRSFYANNHCIGTDLNNSFKWCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 300  
Qy 264 NQIKAYISMHSYSHIYVFPYSYTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHSE 323  
Db 301 NQIKAYISMHSYSHIYVFPYSYTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHSE 360

Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGDDWIYDLGIKYSFT 383  
RESULT 7  
US-08-696-139-2  
; Sequence 2, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hershberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/696,139  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: US 08/153,258  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 404 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-696-139-2  
Query Match 33.5%; Score 640.5; DB 1; Length 404;  
Best Local Similarity 37.7%; Pred. No. 7.8e-61;  
Matches 136; Conservative 60; Mismatches 122; Indels 43; Gaps 6;  
Qy 23 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLMQPVTDLIVKKQVHFVNASVDNVKA 82  
Db 10 FEQEKVPRVNVDENDISLHSLASTRQJDFWKPDSTVQIKPHSTVDFRVKAEDILAVED 69  
Qy 83 HIANVSGIPCSVLLADVDELIOQIISNDTVSPRASASYEQHSLNEIYSWIEFITERHDP 142  
Db 70 FLQNELQYEVLLNNLSRVLEAQFDSRV---RTGHSYKYNWETLEATWKQVTSNP 126  
Qy 143 MLTKIHGSSPEKPYLYVLKVSQKQTAKNAIWIDCGIHAREWISPAFLMFI----- 195  
Db 127 LISRTAIGTTFGLNNIYLLKV-EKPGENTPAI PMDCGFHAREWISHAFQCMFYREAVLTY 185  
Qy 196 -----GH-----NRMRKNSFYANNHCIGTDLNNSFVSK 225  
Db 186 GYSHMTFELNKLDFVYVLPVNLIDGYIYWTQRNMRKTRSTAGTTCIGTDPNRNF-DA 244

Qy 226 HWCBEASSSCSCTCYGLYPESEBPKAVASFLRRNINOIKAYISMHSYSHIVFPYSY 285  
Db 245 GWCTTGASTPCDCTYCGSAASEKETKALADFIRNLSSIKAYLTHSYSQMLYPYSY 304  
Qy 286 TRSKSDHEELSLVASBAVRAIDKTSKNRYTHGHGSETLYLAPGGDDWYDLGIKYSF 345  
Db 305 DYKLPENNAELNLAKAARKEL-ATLYGTYKTYGPGATTIYPAGGSDWAYDQGIKYSF 363  
Qy 346 T 346  
Db 364 T 364  
RESULT 8  
US-08-860-882A-57  
; Sequence 57, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
; APPLICANT: TAREAGONA-PIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-860-882A-57

Query Match 33.4%; Score 639; DB 2; Length 415;  
Best Local Similarity 35.6%; Pred. No. 1.2e-60;  
Matches 135; Conservative 69; Mismatches 131; Indels 44; Gaps 7;  
Qy 6 L AVLPIVLFCQHVFA-FQSGOVLAALPRTSRQOVQLNLTFTTYEIVLMQPVYADLVK 64  
Db 2 LLVLVTVALSAHGGHFGKVRVNVDEHNHIIIRLASTTQIDFWKPDVSTQIKP 61  
Qy 65 KQVHFVNASVDVNDKHAHLNVSGVLLADVEDLIQQOISNDTVSPRASASYEQYH 124

Db 62 HSTVDPRVRAEDTVTVENVLKQELQYKVLISLNRNVBAQFDSRV---RATGHSYEKYN 118  
Qy 125 SLNEIYSWIEFTIERHPDMLTKIHIGSSSEKYPYLYVLKYSQKQTAKNAIWIDGTHARE 184  
Db 119 KWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAIFMDCGFHARE 177  
Qy 185 WISPAFLWFI-----GH-----NRMWRKNSF 207  
Db 178 WISPAFCQFVRAVRYTYGREIQVTELLDKLPVLPVLNIDGYIYTWTKSRFWKTRST 237  
Qy 208 YANNHCIGTDLNSNFVSKHWCEGASSSCSCTCYGLYPESEBPKAVASFLRRNINOIK 267  
Db 238 HTGSSCIGTDPNRF-DAGWCEIGASRNPCDETYCGPAAESEKETKALADFIRNLSSIK 296  
Qy 268 AYISMHSYSHIVFPYSYTRSKSDHEELSLVASBAVRAIDKTSKNRYTHGHGSETLYL 327  
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Qy 328 APGGGDDWYDLGIKYSFT 346  
Db 356 AAGGSDWAYDQGIKYSFT 374  
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US-09-011-769A-39  
; Sequence 39, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKLEY, David C.  
; DAVIES, David H.  
; HENNAM, John P.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-011-769A-39  
Query Match 33.4%; Score 639; DB 4; Length 415;



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; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-7

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Best Local Similarity 37.0%; Pred. No. 1.7e-59;
Matches 140; Conservative 60; Mismatches 131; Indels 47; Gaps 8;

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7 MAVIYTTLAIPVH---FDREKVRVQLQNEKHSVLKNTLSQSLDFWYDPDAIHDAVN 63

Qy 66 KQVHFFNADVDNVKAHLNVSGIPCSVLLADVEDLIQQQIS--NDTVSPRASASYEQQYH 124
Db :||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 MTVDVFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDEIAGRHS---YAKYN 120

Qy 125 SLMEIYSWIEFITERHDPMLTKIHGSSFEKYPVLYLVKVGSKBOTAKNAIWIDCGIHARE 184
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121 DWKIVSWTEKMLEKHPMVSVRIKIGSTVEDNPPLYVLKI--GKKDGERKAIFMDCGIHARE 179

Qy 185 WISPAFLWFI-----GHN-----RWRKNRSF 207
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180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFVLPVFNVDGYIWSWTQDRMWRKNRSR 239

Qy 208 YANNHCIGTDLNSNFVSKHWCCEGASSSCSETYCGLYPSEPEVKAVASFLRNINQIK 267
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
240 NQNSTCIGTDLNRNF--DVSWDSSPNTPKCLNVYRGPAPESEKETKAVTNFIRSHLSNIK 298

Qy 268 AYISMHSYQHIVFPYPTYSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSETLYL 327
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
299 AYITFHSYSQMLLIPYGYTFKLPNPHQDLKQVARIATDAL--STRYETRYIYGPIASTIYK 357

Qy 328 APGGGDDWIYDLGIKYSF 345
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358 TSGSSLDWVYDLGIKHTF 375

RESULT 13
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haeak, Janet E. 28,616
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
US-07-649-591B-6

Query Match 32.4%; Score 619.5; DB 1; Length 417;
Best Local Similarity 34.1%; Pred. No. 1.6e-58;
Matches 130; Conservative 76; Mismatches 128; Indels 47; Gaps 8;

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1 MRLLPVGLIATTLAIAPVRFDRKVERVKPQDEKQADIIDKLAKTNELDFWYFGATHV 60
QY 63 VKKKQVHFFVNASVDVNDVKAHLNVSGIPCSVLLADVEDLIQQOIS-NDTVSPRASASYE 121
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61 AANMVDVFRVSEKESQAIQALDQNKWYELIHDLOEEIEKQFDVKEDIPGRHS---YA 117
QY 122 QYHSLNEIYSWIFETERHPDMLTKIHIGSSFKEYPLYLVKVSQKQAKNAIWIIDCGIH 181
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
118 KYNWEKIVAWTEKMDKPEMVSRKIGSTVEDNPLYVLKI-GEKNERKKAIFMDCGIH 176
QY 182 AREWISPAFLWFI-----GH-----NRMRKN 204
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
177 AREWSPAFQWFYQATKYGRNKIMTKLLDRMNFYILFVFNVDGYINSWTKRMWRKN 236
QY 205 RSPVANNHCIGTDLNSNFVSKHCEEGASSSCSETYCGLYPESEPEVKAVASFLRRNIN 264
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
237 RSKNQSKKICIGTDLNRNF-NASWNSIPNTNDPCADNYRGSAPESEKETKAVTNFIRSHLN 295
QY 265 QIKAYISMHSYSQHIYPPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSET 324
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
296 EIKVYITFHSYSQMLFPFYGYTSKLPENHEDLAKVAKIGTDLV-STRYETRIYGPUEST 354
QY 325 LYLAPGGDDWIYDLGIKYSF 345
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
355 IYPIGSSSLDWAYDLGIKHTF 375
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Search completed: October 28, 2004, 19:47:02  
Job time : 29.4576 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 19:43:44 ; Search time 82.3729 Seconds  
(without alignments)  
1416.943 Million cell updates/sec

Title: US-09-980-881A-2

Perfect score: 1911

Sequence: 1 MKLCSLAVLPVILFCEQHV.....IKYFTSNPPVEXLLPLSLK 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1817	95.1	386	9	US-09-813-133A-2
2	1817	95.1	386	14	US-10-212-877-2
3	1799.5	94.2	423	14	US-10-379-836-17
4	1788.5	93.6	423	9	US-09-813-133A-4
5	1788.5	93.6	423	14	US-10-212-877-4
6	1776	92.9	428	15	US-10-115-479-68
7	1776	92.9	428	15	US-10-115-479-70
8	1716.5	89.8	423	14	US-10-379-836-2
9	1528	80.0	422	14	US-10-379-836-18
10	1499	78.4	422	14	US-10-379-836-16
11	1407	73.6	322	15	US-10-115-479-64
12	1361	71.2	354	15	US-10-115-479-66
13	803.5	42.0	211	9	US-09-925-302-467

14	803.5	42.0	211	10	US-09-925-302-467	Sequence 467, App
15	646	33.8	416	15	US-10-074-978A-269	Sequence 269, App
16	641	33.5	417	15	US-10-074-978A-267	Sequence 267, App
17	641	33.5	417	15	US-10-074-978A-268	Sequence 268, App
18	641	33.5	417	16	US-10-477-515-3	Sequence 3, Appli
19	631.5	33.0	402	14	US-10-379-836-20	Sequence 20, Appl
20	627	32.8	416	15	US-10-074-978A-270	Sequence 270, App
21	623	32.6	716	9	US-09-910-059-125	Sequence 125, App
22	621.5	32.5	416	15	US-10-074-978A-266	Sequence 266, App
23	619.5	32.4	417	14	US-10-229-546-2	Sequence 2, Appli
24	619.5	32.4	417	14	US-10-229-546-9	Sequence 9, Appli
25	619.5	32.4	417	14	US-10-341-434-188	Sequence 188, App
26	619.5	32.4	417	15	US-10-262-511-72	Sequence 72, Appl
27	604	31.6	434	16	US-10-477-515-2	Sequence 10, Appl
28	604	31.6	437	13	US-10-200-344-10	Sequence 12, Appl
29	604	31.6	437	14	US-10-274-639-12	Sequence 12, Appl
30	604	31.6	437	15	US-10-333-574-12	Sequence 128, App
31	602	31.5	437	17	US-10-757-262-128	Sequence 61, Appl
32	563	29.5	374	9	US-09-888-615-61	Sequence 74, Appl
33	563	29.5	444	14	US-10-176-306-74	Sequence 8, Appli
34	546	28.6	399	14	US-10-200-910-8	Sequence 8, Appli
35	546	28.6	399	17	US-10-843-130-8	Sequence 113, App
36	543	28.4	613	9	US-09-910-059-113	Sequence 4, Appli
37	543	28.4	613	16	US-10-608-710-4	Sequence 788, App
38	533.5	27.9	419	15	US-10-072-012-788	Sequence 12, Appl
39	528.5	27.7	350	13	US-10-200-344-12	Sequence 887, App
40	522	27.3	286	15	US-10-072-012-887	Sequence 40, Appl
41	519.5	27.2	419	15	US-10-257-174-40	Sequence 6, Appli
42	519.5	27.2	436	14	US-10-200-910-6	Sequence 316, App
43	519.5	27.2	436	15	US-10-072-012-316	Sequence 784, App
44	519.5	27.2	436	15	US-10-072-012-784	Sequence 39, Appl
45	519.5	27.2	436	15	US-10-257-174-39	

ALIGNMENTS

RESULT 1

US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: US9813133A  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 95.1%; Score 1817; DB 9; Length 386;  
Best Local Similarity 98.6%; Pred. No. 1e-169;  
Matches 341; Conservative 1; Mismatches 4; Indels 0; Gaps 0;



QY 61 LIVKKQVHFVNADVDNKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASYY 120  
DB 61 LIVKKQVHFVNADVDNKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASYY 120  
QY 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKPYLYLVKVGSGQTAQNAIWDGCI 180  
DB 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKPYLYLVKVGSGQTAQNAIWDGCI 180  
QY 181 HAREWISPAFLCWIGH-----NRWRK 203  
DB 181 HAREWISPAFLCWIGHITQYIGIQTNLLRLVDFYVMPVNVVDGYDYSWKQNRWRK 240  
QY 204 NRSFYANNHCIGTDLNFSKWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
DB 241 NRSFYANNHCIGTDLNRFASKWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 300  
QY 264 NOIKAYISMYSQHIYVFPYSYTRSKSKDHELSLVAEAVRAIDKTSKNTRYTHGHGSE 323  
DB 301 NOIKAYISMYSQHIYVFPYSYTRSKSKDHELSLVAEAVRAIEKISKNTRYTHGHGSE 360  
QY 324 TLYLAPGGDDWIYDLGIKYSFT 346  
DB 361 TLYLAPGGDDWIYDLGIKYSFT 383  
RESULT 5  
US-10-212-877-4  
; Sequence 4, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinlu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173D1V  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
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Query Match 93.6%; Score 1788.5; DB 14; Length 423;  
Best Local Similarity 89.0%; Pred. No. 7.3e-167;  
Matches 341; Conservative 1; Mismatches 4; Indels 37; Gaps 1;  
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DB 1 MKLCSLAVLPVILFCQHVAFQSGVLAALPRTSRQVQLQNLTTTYIVLWQPVTD 60  
QY 61 LIVKKQVHFVNADVDNKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASYY 120  
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DB 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKPYLYLVKVGSGQTAQNAIWDGCI 180  
QY 181 HAREWISPAFLCWIGH-----NRWRK 203  
DB 181 HAREWISPAFLCWIGHITQYIGIQTNLLRLVDFYVMPVNVVDGYDYSWKQNRWRK 240  
QY 204 NRSFYANNHCIGTDLNFSKWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
DB 241 NRSFYANNHCIGTDLNRFASKWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 300  
QY 264 NOIKAYISMYSQHIYVFPYSYTRSKSKDHELSLVAEAVRAIDKTSKNTRYTHGHGSE 323  
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RESULT 6  
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; Sequence 68, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 68  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-68  
Query Match 92.9%; Score 1776; DB 15; Length 428;  
Best Local Similarity 87.9%; Pred. No. 1.3e-165;



ORGANISM: Papio hamadryas  
US-10-379-836-2

Query Match 89.8%; Score 1716.5; DB 14; Length 423;  
Best Local Similarity 85.4%; Pred. No. 8.9e-160; Mismatches 12; Indels 37; Gaps 1;  
Matches 327; Conservative 7;

Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVAD 60  
Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVAD 60

Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVDELIOQQISNDTVSPRASASY 120  
Db 61 LIEKKQVHFFVNSSDVNDVNVKAHLNVSGIPCSVLLADVDELIOQQISNDTVSPRASASY 120

Qy 121 EQYHSLNEIYSWIEFITERPDMLTKIHGSSPEKPYLVLVKSGKEQAKNAIWDGCI 180  
Db 121 EQYHSLNEIYSWIELEITEKYPDMLTKIHGSSYEKHPYLVLVKSGKEQAKNAIWDGCI 180

Qy 181 HAREWISPAFLWFIGH-----NRMWRK 203  
Db 181 HAREWISPAFLWFIGHITEYGIIGETYNLLRHVDYFVMPVNVVDGYDYSWKKNRMWRK 240

Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 241 NRSFYANNRCITGTDLRNFASFASKHWCCEGASSFSCTYCGLYPESEPEKAVANFLRNI 300

Qy 264 NOIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 301 NHIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAIQKTSKNIRYTHGHGSE 360

Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 361 TLYLAPGGADWIYDLGIKYSFT 383

RESULT 9  
US-10-379-836-18  
; Sequence 18, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-379-836-18

Query Match 80.0%; Score 1528; DB 14; Length 422;  
Best Local Similarity 76.2%; Pred. No. 3.1e-141;  
Matches 292; Conservative 24; Mismatches 29; Indels 38; Gaps 2;

Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVAD 60  
Db 1 MKLHGLILVAILLY-EKHGLAFQSGHLSALPRTSRQVQLQNLTTTYEIVLWQPVAD 59

Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVDELIOQQISNDTVSPRASASY 120  
Db 60 FIEKKQVHFFVNASDVSDSKAHLNVSRIPFVLMNVDELIEQQTNDTVSPRASASY 119

Qy 121 EQYHSLNEIYSWIEFITERPDMLTKIHGSSPEKPYLVLVKSGKEQAKNAIWDGCI 180  
Db 120 EQYHSLNEIYSWIEITEQHPDMLQKIYIGSSPEKPYLVLVKSGKEHVRKNAIWDGCI 179

Qy 181 HAREWISPAFLWFIGH-----NRMWRK 203  
Db 180 HAREWISPAFLWFIGHYVTFQPHCKENTYTLRLRHVDYFVMPVNVVDGYDYSWKKNRMWRK 239

Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 240 NRSVHMNNRCVGTDLNRNFASFASKHWCCEGASSFSCTYCGLYPESEPEVKAVADFLRNI 299

Qy 264 NOIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 300 NHIKAYISMHSYSOQLFPYSYTRSKSKDHEELSLVASEAVRAIESINKNTRYTHGHGSE 359

Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 360 SLYLAPGGDDWIYDLGIKYSFT 382

RESULT 11  
US-10-115-479-64

Qy 181 HAREWISPAFLWFIGH-----NRMWRK 203  
Db 180 HAREWISPAFLWFIGHYVTFQPHCKENLYTLRLRHVDYFVMPVNVVDGYDYSWKKNRMWRK 239

Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 240 NRSAHKNNRCVGTDLNRNFASFASKHWCCEGASSFSCTYCGLYPESEPEVKAVADFLRNI 299

Qy 264 NOIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 300 DHIKAYISMHSYSOQLFPYSYTRSKSKDHEELSLVASEAVRAIESINKNTRYTHGHGSE 359

Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 360 SLYLAPGGDDWIYDLGIKYSFT 382

RESULT 10  
US-10-379-836-16  
; Sequence 16, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-379-836-16

Query Match 78.4%; Score 1499; DB 14; Length 422;  
Best Local Similarity 74.7%; Pred. No. 2.2e-138;  
Matches 286; Conservative 26; Mismatches 33; Indels 38; Gaps 2;

Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVAD 60  
Db 1 MKLYGLGLVAILLY-EKHGLAFQSGHLSALPRTSRQVQLQNLTTTYEIVLWQPVAD 59

Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVDELIOQQISNDTVSPRASASY 120  
Db 60 FIEKKQVHFFVNASDVNSVKAYLNASRIPFVLMNVDELIOQQTSNDTVSPRASASY 119

Qy 121 EQYHSLNEIYSWIEFITERPDMLTKIHGSSPEKPYLVLVKSGKEQAKNAIWDGCI 180  
Db 120 EQYHSLNEIYSWIEITEQHPDMLQKIYIGSSYEKPYLVLVKSGKEHVRKNAIWDGCI 179

Qy 181 HAREWISPAFLWFIGH-----NRMWRK 203  
Db 180 HAREWISPAFLWFIGHYVTFQPHCKENTYTLRLRHVDYFVMPVNVVDGYDYSWKKNRMWRK 239

Qy 204 NRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRNI 263  
Db 240 NRSVHMNNRCVGTDLNRNFASFASKHWCCEGASSFSCTYCGLYPESEPEVKAVADFLRNI 299

Qy 264 NOIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTHGHGSE 323  
Db 300 NHIKAYISMHSYSOQLFPYSYTRSKSKDHEELSLVASEAVRAIESINKNTRYTHGHGSE 359

Qy 324 TLYLAPGGDDWIYDLGIKYSFT 346  
Db 360 SLYLAPGGDDWIYDLGIKYSFT 382

RESULT 11  
US-10-115-479-64

```
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Query Match 73.6%; Score 1407; DB 15; Length 322;
Best Local Similarity 80.6%; Pred. No. 1.6e-129;
Matches 279; Conservative 1; Mismatches 2; Indels 64; Gaps 1;

Qy 1 MKLCSLAVLVIVLFCFCEQHVAFQSGQVLAALPRTSRQVQLQNIITTYEIVLWQPVTAD 60
Db 1 MKLCSLAVLVIVLFCFCEQHVAFQSGQVLAALPRTSRQVQLQNIITTYEIVLWQPVTAD 60

Qy 61 LIVKKQVHFFVNADSDVNVKAHLNVSGIPCSVLLADVEDIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNADSDVNVKAHLNVSGIPCSVLLADVEDIQQOISNDTVSPRASASY 120
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Qy 121 EQYHSLNEIYSWIEFTTERHPDMLTKIHGSSPEKYPLVYLKYSKEQTAKNAIWDCGI 180
Db 121 EQYHSLNEIYSWIEFTTERHPDMLTKIHGSSPEKYPLVYLKYSKEQTAKNAIWDCGI 177
Qy 181 HAREWISPAFCLWFIQHNRMRKNRSFYANNHCIGTDLNSNFVSKHWCERGASSSCSET 240
Db 178 -----
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAIISMHSYQSHIVFPYSTRSKSKDHEELSLVA 300
Db 178 -CGLYPESEPEVKAVASFLRRNINQIKAIISMHSYQSHIVFPYSTRSKSKDHEELSLVA 236
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLACGGDDWIYDLGIKYSFT 346
Db 237 SEAVRAIEKISKNTRYTHGHGSETLYLACGGDDWIYDLGIKYSFT 282
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## RESULT 12

```
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
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; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match      71.2%; Score 1361; DB 15; Length 354;
Best Local Similarity 69.3%; Pred. No. 6.3e-125;
Matches 269; Conservative 0; Mismatches 3; Indels 116; Gaps 3;

Qy 1 MKLCSLAVLPVIVLFCRQHFVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPTAD 60
Db 1 MKLCSLAVLPVIVLFCRQHFVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPTAD 60

Qy 61 LIVKKQVHFVNASDVNDVNVKAHLNVSIGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Db 61 LIVKKQVHFVNASDVNDVNVKAHLNVSIGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120

Qy 121 EOVHSLNEIYSWIEFITERPDMLTKIIGSSPEKYPYLVK-----VSGKEQTAKNAIW 175
Db 121 EOVHSLNEIYSWIEFITERPDMLTKIIGSSPEKYPYLVK-----VSGKEQTAKNAIW 180

Qy 176 IDCIIHAREWISPAFLWFIH-----N 198
Db 181 IDCIIHAREWISPAFLWFIHITQFYIIGQYTNLLRLVDVFPVWVNDGYDSWKN 240

Qy 199 RMRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSCSETYCGLYPESEPEVKAASF 258
Db 241 RMRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSETYCGLYPE----- 289

Qy 259 LRNNIQIKAYISMHSYSHIVFPYSYTRSKSKDHEELSLVASEAVRAIDKTSKNTRYTH 318
Db 290 ----- 289

Qy 319 GHGSETLYLAPGGDDWIYDLGIKYSFT 346
Db 290 ---SETLYLAPGGDDWIYDLGIKYSFT 314

RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match      42.0%; Score 803.5; DB 9; Length 211;
Best Local Similarity 88.8%; Pred. No. 2e-70;
Matches 151; Conservative 2; Mismatches 8; Indels 9; Gaps 2;

Qy 185 WISPAFLWFI-----GHNRMRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSS 236
Db 3 WIS-MLCRWLMMVMNYSWKKNRMRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSS 61

Qy 237 CSETYCGLYPESEPEVKAFLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKDHEEL 296
Db 62 CSETYCGLYPESEPEVKAFLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKDHEEL 121

Qy 297 SLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 346
Db 122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
```

```
Db 62 CSETYCGLYPESEPEVKAFLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKDHEEL 121

Qy 297 SLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 346
Db 122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match      42.0%; Score 803.5; DB 10; Length 211;
Best Local Similarity 88.8%; Pred. No. 2e-70;
Matches 151; Conservative 2; Mismatches 8; Indels 9; Gaps 2;

Qy 185 WISPAFLWFI-----GHNRMRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSS 236
Db 3 WIS-MLCRWLMMVMNYSWKKNRMRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSS 61

Qy 237 CSETYCGLYPESEPEVKAFLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKDHEEL 296
Db 62 CSETYCGLYPESEPEVKAFLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKDHEEL 121

Qy 297 SLVASEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 346
Db 122 SLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
```

APPLICANT: Pena, Carol E A  
APPLICANT: Shimkets, Richard A  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Moore, No. US20040010119A11e  
APPLICANT: Shenoy, Suresh  
APPLICANT: Edinger, Shlomit  
APPLICANT: Gunther, Erik  
APPLICANT: Stone, Dave  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-269  
CURRENT APPLICATION NUMBER: US/10/074, 978A  
CURRENT FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: 60/268,221  
PRIOR FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/335,109  
PRIOR FILING DATE: 2001-10-31  
PRIOR APPLICATION NUMBER: 60/312,284  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: 60/268,496  
PRIOR FILING DATE: 2001-02-13  
PRIOR APPLICATION NUMBER: 60/276,703  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/330,293  
PRIOR FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 60/322,127  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/280,899  
PRIOR FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: 60/310,797  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/268,646  
PRIOR FILING DATE: 2001-02-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 269  
LENGTH: 416  
TYPE: PRT  
ORGANISM: Sus scrofa  
US-10-074-978A-269

Query Match 33.8%; Score 646; DB 15; Length 416;  
Best Local Similarity 36.6%; Pred. No. 1.7e-54;  
Matches 140; Conservative 64; Mismatches 134; Indels 44; Gaps 7;  
Qy 3 LCSLAVLPVILFCEQHVFA-FQSGQVLAALPRTSRQVQVLQNLTTTVEIWLWOPVTADL 61  
Db 1 MLAFILITVTTLASAHSGHEFGEKVPFVNVEDENDISLHLASTRQIDFWKPDSTQ 60  
Qy 62 IVKKKQVHFFVNADVNVAHLNVSGIPCSVLADVEDLIQQQISNDTVSPRASASYE 121  
Db 61 IKPHSTVDVRKAEDILAVEDFLQNELQVEVLNNLSVLEAQFDSRV---RTTGHSYE 117  
Qy 122 QYHSLNEIYSWIEFTETHPDMLTKIHIGSFEKYPYLVKVSKEQTAKNAIWDGCIH 181  
Db 118 KYNWETTEAWTKQVTSNPDLISRTAIGTTLGNNIYLLKV-GKPGPNKPAIFMDCGFH 176  
Qy 182 AREWISPAFCLEWFI-----GH-----NRMWRKN 204  
Db 177 AREWISHAFQWVFREAVLTGYGSHMTEFLNKLDFFYLPVLINIDGYIYTTKRMWRKT 236  
Qy 205 RSFYANNHCIGTDLNSNFVSKHCEGASSSCSETCGLYPESEPEVKAVASFLRRNIN 264  
Db 237 RSTNAGTTCIGTDPNRF-DAGWCTTGASTDPCDETCGSAASEKETKALADFI RNLS 295  
Qy 265 QIKAYISMHSYSQHIVFPYSYTRSKSKDHELSLVASEAVRAIDKTSKNTRYTHGHSET 324  
Db 296 SIKAYLTIHSYSQMLYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTYTYPGATT 354  
Qy 325 LYLAPGGGDDWIYDLGIKYSFT 346

Db 355 IYPAAGSDDWAYDQGIKYSFT 376  
Search completed: October 28, 2004, 20:05:50  
Job time : 83.3729 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:35:31 ; Search time 333.305 Seconds  
(without alignments)  
1196.740 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 1911  
Sequence: 1 MKLCSLAVLPIVLFCRQHV.....IKYSFTSNPPVKKLLPLSLK 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1911	100.0	360	25	US-09-980-881-2	Sequence 2, Appli
2	1911	100.0	360	27	US-09-980-881A-2	Sequence 2, Appli
3	1886	98.7	360	25	US-10-170-205E-13306	Sequence 13306, A
4	1886	98.7	360	34	US-10-803-180-126	Sequence 126, App
5	1886	98.7	360	35	US-10-918-754-1941	Sequence 1941, Ap
6	1886	98.7	360	36	US-60-452-680-21530	Sequence 21530, A
7	1886	98.7	360	36	US-60-453-050-13037	Sequence 13037, A
8	1886	98.7	360	36	US-60-453-133-13037	Sequence 13037, A
9	1886	98.7	360	36	US-60-455-444-6989	Sequence 6989, Ap
10	1886	98.7	360	36	US-60-465-241-6989	Sequence 6989, Ap
11	1886	98.7	360	36	US-60-466-413-13037	Sequence 13037, A
12	1886	98.7	360	36	US-60-495-114-1941	Sequence 1941, Ap
13	1886	98.7	366	24	US-09-949-003C-3190	Sequence 3190, Ap
14	1886	98.7	366	24	US-09-949-003C-3191	Sequence 3191, Ap
15	1884	98.6	360	22	US-09-791-537-142876	Sequence 142876, A
16	1884	98.6	360	24	US-09-949-003C-2616	Sequence 2616, Ap
17	1818	95.1	386	1	PCT-US03-31531-18	Sequence 18, Appli
18	1817	95.1	386	1	PCT-US02-08289-2	Sequence 2, Appli
19	1817	95.1	386	28	US-10-212-877-2	Sequence 2, Appli
20	1799.5	94.2	423	1	PCT-US03-26773-2	Sequence 2, Appli
21	1799.5	94.2	423	3	US-07-959-944A-3	Sequence 3, Appli
22	1799.5	94.2	423	22	US-09-791-537-96834	Sequence 96834, A
23	1799.5	94.2	423	24	US-09-949-003C-2062	Sequence 2062, Ap
24	1799.5	94.2	423	29	US-10-379-836-17	Sequence 17, Appli
25	1799.5	94.2	423	30	US-10-486-034-2	Sequence 2, Appli
26	1799.5	94.2	423	36	US-60-353-790-3726	Sequence 3726, Ap
27	1799.5	94.2	423	36	US-60-361-523-17	Sequence 17, Appli
28	1794.5	93.9	423	27	US-10-170-205E-13305	Sequence 13305, A
29	1794.5	93.9	423	34	US-10-803-180-127	Sequence 127, App
30	1794.5	93.9	423	35	US-10-918-754-1942	Sequence 1942, Ap
31	1794.5	93.9	423	36	US-60-452-680-21529	Sequence 21529, A
32	1794.5	93.9	423	36	US-60-453-050-13036	Sequence 13036, A
33	1794.5	93.9	423	36	US-60-455-444-6988	Sequence 6988, Ap
34	1794.5	93.9	423	36	US-60-465-241-6988	Sequence 13036, A
35	1794.5	93.9	423	36	US-60-466-412-13036	Sequence 13036, A
36	1794.5	93.9	423	36	US-60-495-114-1942	Sequence 1942, Ap
37	1794.5	93.9	423	36	US-09-949-003C-3188	Sequence 3188, Ap
38	1794.5	93.9	429	24	US-09-949-003C-3189	Sequence 3189, Ap
39	1794.5	93.9	429	24	US-09-949-003C-3189	Sequence 3189, Ap
40	1788.5	93.6	423	1	PCT-US02-08289-4	Sequence 4, Appli
41	1788.5	93.6	423	28	US-10-212-877-4	Sequence 4, Appli
42	1786.5	93.5	424	22	US-09-760-475-1824	Sequence 1824, Ap
43	1786.5	93.5	424	28	US-10-227-425-1824	Sequence 1824, Ap
44	1785	93.4	338	25	US-09-980-881-3	Sequence 3, Appli
45	1785	93.4	338	25	US-09-980-881A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-980-881-2  
; Sequence 2, Application US/09980881  
; GENERAL INFORMATION:  
; APPLICANT: AKIRA MATSUMOTO  
; TITLE OF INVENTION: Human Brain Carboxypeptidase B  
; FILE REFERENCE: MAT-101PCT  
; CURRENT APPLICATION NUMBER: US/09/980,881  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-980-881-2

Query Match 100.0%; Score 1911; DB 25; Length 360;

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Best Local Similarity 100.0%; Pred. No. 2.2e-192; Mismatches 0; Indels 0; Gaps 0;
Matches 360; Conservative 0;

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Db 61 LIVKKQVHFVNADVDNVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180

Qy 181 HAREWISPAFCMLWFIHNRMRKNSFYANNHCIGTDLNSFVSKHWCCEGASSSCSET 240
Db 181 HAREWISPAFCMLWFIHNRMRKNSFYANNHCIGTDLNSFVSKHWCCEGASSSCSET 240

Qy 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300

Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 2
US-09-980-881a-2
; Sequence 2, Application US/09980881a
; GENERAL INFORMATION:
; APPLICANT: AKIRA MATSUMOTO
; TITLE OF INVENTION: Human Brain Carboxypeptidase B
; FILE REFERENCE: MAT-101PCT
; CURRENT APPLICATION NUMBER: US/09/980,881A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: JP 1999-125169
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-980-881a-2

Query Match 100.0%; Score 1911; DB 25; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.2e-192;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LIVKKQVHFVNADVDNVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180

Qy 181 HAREWISPAFCMLWFIHNRMRKNSFYANNHCIGTDLNSFVSKHWCCEGASSSCSET 240
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Qy 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300

Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 3
US-10-170-205E-13306
; Sequence 13306, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCES: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13306
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-13306

Query Match 98.7%; Score 1866; DB 27; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60

Qy 61 LIVKKQVHFVNADVDNVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120
Db 61 LIVKKQVHFVNADVDNVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKYPYLVKVGSKQAKNAIWDGCI 180

Qy 181 HAREWISPAFCMLWFIHNRMRKNSFYANNHCIGTDLNSFVSKHWCCEGASSSCSET 240
Db 181 HAREWISPAFCMLWFIHNRMRKNSFYANNHCIGTDLNSFVSKHWCCEGASSSCSET 240

Qy 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIYVPYSTRSKSKDHEELSLVA 300

Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 4
US-10-803-180-126
; Sequence 126, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCES: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-180-126

Query Match 98.7%; Score 1836; DB 34; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 121 EQHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKVGSGEQTAKNAIWDGCI 180
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Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVA 300
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Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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## RESULT 5

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US-10-918-754-1941
; Sequence 1941, Application US/10918754
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: CODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/10/918,754
; CURRENT FILING DATE: 2004-08-16
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1941
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-918-754-1941
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Query Match 98.7%; Score 1886; DB 35; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
Qy 61 LIVKKQVHFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASYY 120
Db 61 LIVKKQVHFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASYY 120
Qy 121 EQHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKVGSGEQTAKNAIWDGCI 180
Db 121 EQHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKVGSGEQTAKNAIWDGCI 180
Qy 181 HAREWISPAFCMLFPIGHNRMWRKRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Db 181 HAREWISPAFCMLFPIGHNRMWRKRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVA 300
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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## RESULT 6

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US-60-452-680-21530
; Sequence 21530, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21530
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-21530
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Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
Qy 61 LIVKKQVHFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASYY 120
Db 61 LIVKKQVHFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQIISNDTVSPRASYY 120
Qy 121 EQHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKVGSGEQTAKNAIWDGCI 180
Db 121 EQHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKVGSGEQTAKNAIWDGCI 180
Qy 181 HAREWISPAFCMLFPIGHNRMWRKRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Db 181 HAREWISPAFCMLFPIGHNRMWRKRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVA 300
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Db 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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## RESULT 7

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US-60-453-050-13037
; Sequence 13037, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13037
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13037
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Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
Db 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
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QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
QY 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
DB 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
QY 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
DB 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
QY 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
DB 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 8
US-60-453-135-13037
; Sequence 13037, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453.135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13037
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13037

Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
QY 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
DB 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
QY 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
DB 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
QY 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
DB 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 9
US-60-455-444-6989
; Sequence 6989, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455.444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6989
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-6989

Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
QY 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
DB 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
QY 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
DB 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
QY 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
DB 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 10
US-60-465-241-6989
; Sequence 6989, Application US/60465241
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001468
; CURRENT APPLICATION NUMBER: US/60/465.241
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 258418
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6989
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-465-241-6989

Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTAD 60
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPYLVKVSKEQTAKNAIWDGCI 180
QY 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
DB 181 HAREWISPAFLWFIHNRMRKNSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
QY 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
DB 241 YCGLYPESEPEVKAVASFLRRNIQIKAYISMHSYQHIYVPPYSYTRSKSKDHEELSLVA 300
QY 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
DB 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
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Db 11 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Qy 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Db 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360

RESULT 11
US-60-466-412-13037
; Sequence 13037, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13037
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-13037

Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60
Db 1 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60
Qy 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Db 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Qy 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Db 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360

RESULT 12
US-60-495-114-1941
; Sequence 1941, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
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```
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CU001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1941
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1941

Query Match 98.7%; Score 1886; DB 36; Length 360;
Best Local Similarity 98.6%; Pred. No. 9.9e-190;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60
Db 1 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60
Qy 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Db 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYLVKSGKEQTAQNAIWDCCI 180
Qy 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Db 181 HAREWISPAFLWFIHGNRMWRKNRSFYANNHCIGTDLNSNFVSKHWCCEGASSSSCSET 240
Qy 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Db 241 YCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360
Db 301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSVTSNPPVEKLLPLSLK 360

RESULT 13
US-09-949-003C-3190
; Sequence 3190, Application US/09949003C
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU000791
; CURRENT APPLICATION NUMBER: US/09/949,003C
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,446
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 74065
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3190
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-003C-3190

Query Match 98.7%; Score 1886; DB 24; Length 366;
Best Local Similarity 98.6%; Pred. No. 1e-189;
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 60
Db 7 MKLCSLAVLPVLPVLFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTAD 66
Qy 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQIISNDTVSPRASYY 120
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Db 67 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASASY 126  
Qy 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQTAKNAIWDGCI 180  
Db 127 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQAANKAIWDGCI 186  
Qy 181 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNSNFVSKHWCERGASSSSCSET 240  
Db 187 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNRFASKHWCERGASSSSCSET 246  
Qy 241 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300  
Db 247 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 306  
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360  
Db 307 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSVTSPNPVEKLLPLSLK 366

RESULT 14  
US-09-949-003C-3191  
; Sequence 3191, Application US/09949003C  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC  
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO00791  
; CURRENT APPLICATION NUMBER: US/09/949,003C  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,446  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 74065  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3191  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-949-003C-3191

Query Match 98.7%; Score 1886; DB 24; Length 366;  
Best Local Similarity 98.6%; Pred. No. 1e-189;  
Matches 355; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60  
Db 7 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 66  
Qy 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASASY 120  
Db 67 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASASY 126  
Qy 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQTAKNAIWDGCI 180  
Db 127 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQAANKAIWDGCI 186  
Qy 181 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNSNFVSKHWCERGASSSSCSET 240  
Db 187 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNRFASKHWCERGASSSSCSET 246  
Qy 241 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300  
Db 247 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 306  
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360  
Db 307 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSVTSPNPVEKLLPLSLK 366

RESULT 15  
US-09-791-537-142876  
; Sequence 142876, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 142876  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-142876

Query Match 98.6%; Score 1884; DB 22; Length 360;  
Best Local Similarity 98.3%; Pred. No. 1.6e-189;  
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60  
Qy 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASASY 120  
Db 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVDELIOQOISNDTVSPRASASY 120  
Qy 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQTAKNAIWDGCI 180  
Db 121 EQYHSLNEIYSWIEFITERHPDMLTKIHGSSPEKPYLYVLKVSQKEQAANKAIWDGCI 180  
Qy 181 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNSNFVSKHWCERGASSSSCSET 240  
Db 181 HAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNRFASKHWCERGASSSSCSET 240  
Qy 241 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300  
Db 241 YCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSYTRSKSKDHEELSLVA 300  
Qy 301 SEAVRAIDKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360  
Db 301 SEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

Search completed: October 28, 2004, 20:01:43  
Job time : 335.305 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 03:40:54 ; Search time 104.873 Seconds  
(without alignments)  
2439.944 Million cell updates/sec

Title: US-09-980-881A-2

Perfect score: 1911

Sequence: 1 MKLCSLAVPLVILFCEQHV.....IKYSFTSNPPVKLLPLSLK 360

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1849.5	96.8	1625	2	US-09-813-133A-1
2	1832	95.9	1272	4	US-08-869-057-1
3	1832	95.9	1749	1	US-07-649-591B-2
4	1832	95.9	1749	1	US-08-277-540-2
5	1832	95.9	1749	1	US-08-430-787A-2
6	640.5	33.5	1215	1	US-08-696-139-1
7	639	33.4	1263	2	US-08-860-882A-56
8	639	33.4	1263	4	US-09-011-769A-38
9	631.5	33.0	1284	2	US-08-860-882A-71
10	631.5	33.0	1284	4	US-09-011-769A-55
11	623	32.6	2154	3	US-09-171-945-124
12	619.5	32.4	1622	4	US-09-023-655-1020

13	611.5	32.0	1311	4	US-09-675-305-9	Sequence 9, Appli
14	611.5	32.0	1311	4	US-10-200-344-9	Sequence 9, Appli
15	604	31.6	927	2	US-08-782-760-5	Sequence 5, Appli
16	604	31.6	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	576	30.1	921	1	US-08-696-139-3	Sequence 3, Appli
18	564	29.5	2128	4	US-09-675-305-13	Sequence 13, Appli
19	564	29.5	2128	4	US-10-200-344-13	Sequence 13, Appli
20	561	29.4	999	2	US-08-860-882A-67	Sequence 67, Appli
21	561	29.4	999	2	US-09-011-769A-50	Sequence 50, Appli
22	561	29.4	1053	2	US-08-860-882A-64	Sequence 64, Appli
23	561	29.4	1053	4	US-09-011-769A-46	Sequence 46, Appli
24	554	29.0	1053	4	US-09-463-451-27	Sequence 27, Appli
c	554	29.0	1053	4	US-09-463-451-28	Sequence 28, Appli
26	554	29.0	1059	2	US-08-860-882A-74	Sequence 74, Appli
27	554	29.0	1059	2	US-09-011-769A-59	Sequence 59, Appli
28	553	28.9	1059	2	US-08-860-882A-77	Sequence 77, Appli
29	553	28.9	1059	4	US-09-011-769A-63	Sequence 63, Appli
30	546	28.6	1200	4	US-09-710-099-7	Sequence 7, Appli
31	546	28.6	1200	4	US-10-200-910-7	Sequence 7, Appli
32	543	28.4	1870	3	US-09-171-945-112	Sequence 112, App
33	528.5	27.7	1050	4	US-09-675-305-11	Sequence 11, Appli
34	528.5	27.7	1050	4	US-10-200-344-11	Sequence 11, Appli
35	519.5	27.2	1311	4	US-09-710-099-5	Sequence 5, Appli
36	519.5	27.2	1311	4	US-10-200-910-5	Sequence 5, Appli
37	513	26.8	1251	3	US-08-640-906-3	Sequence 3, Appli
38	513	26.8	1251	3	US-09-395-936-3	Sequence 3, Appli
39	487.5	25.5	1257	3	US-08-640-906-1	Sequence 1, Appli
40	487.5	25.5	1257	3	US-09-395-936-1	Sequence 1, Appli
41	460.5	24.1	945	4	US-09-710-099-3	Sequence 3, Appli
42	460.5	24.1	945	4	US-09-710-099-11	Sequence 11, Appli
43	460.5	24.1	945	4	US-10-200-910-3	Sequence 3, Appli
44	460.5	24.1	945	4	US-10-200-910-11	Sequence 11, Appli
45	458.5	24.0	2247	4	US-09-710-099-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1

US-09-813-133A-1

; Sequence 1, Application US/09813133A

; Patent No. 6455294

; GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CLO01173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1625

; TYPE: DNA

; ORGANISM: Human

US-09-813-133A-1

Alignment Scores:

Pred. No.: 6.66e-227 Length: 1625  
Score: 1849.50 Matches: 355  
Percent Similarity: 94.18% Conservative: 1  
Best Local Similarity: 93.92% Mismatches: 4  
Query Match: 96.78% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy	1	MetLysLeuCysSerLeuAlaValLeuValProfileValLeuPheCysGluGlnHisVal	20
Db	17	ATGAGCTTGGACCTTCGAGTCCCTTGACCATTTCTCTCTGTGAGCAGCATGTC	76
Qy	21	PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln	40



Db 77 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTCTTCTCTAGAACCTCTAGGCAAGTTCAA 136  
Qy 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGAATCTTACTACAACATATGAGATTGTTCTTGGCAGCGGGTAACAGCTGAC 196  
Qy 61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
Db 197 CTTATTGTGAAGAAAAACCAAGTCCATTTTTTTGTAATGCAATCTGATGTGCAAAATGTG 256  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCATTAAATGAGGGGAATTCATGCAATGCTTTGCTGGCAGATGTGGAAGAT 316  
Qy 101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTCCAAACGACACAGTACAGCCCGAGCCCTCGCATGCTACTAT 376  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAAATCTATTCTTTGGATAGAATTTATAACTGAGAGCAT 436  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CCTGATATGCTTACAAAATCCAAATGGATGCTTCNTTGGAAAGTACCCACTATATGTT 496  
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
Db 497 TTAAGGTTTCTGAAAGAAACAAAGCAGCCAAAAATGCCATATGATGATGCTGGAAATC 556  
Qy 181 HisLargGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Db 557 CATGCCAGAGAATGGATCTCTCTGCTTCTGCTTGTGGTTCATAGGCCCAATAATCGAATG 616  
Qy 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220  
Db 617 TGGAGAAAGAACCGTTCCTTCTATGCGAACAAATCATTTGTCATCGGAACAGACTGAAATAGG 676  
Qy 221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
Db 677 AACTTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACC 736  
Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Db 737 TACTGTGACATTTATCTCTAGTCAAGAACCAAGAGTGAAGCGAGTGGCTAGTTCTTGAGA 796  
Qy 261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280  
Db 797 AGAATATCAACCAAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 856  
Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
Db 857 TTTCCATATTCCTATACAGGAATGAAAGCAAGCAACCATGAGGAACCTGCTCTAGTAGCC 916  
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320  
Db 917 AGTGAAGCAGTTCTGCTGCTATTGAGAAAATTAAGTAAAAATACAGGTATACACATGGCCAT 976  
Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 340  
Db 977 GGCTCAGNAACCTTATACCTAGTCTCTGGAGGTGGGACGATGGATCTATGATTTGGGC 1036  
Qy 341 IleLysTyrSerPhe----- 345  
Db 1037 ATCAAAATTCGTTTACAAATTTGAACCTTCGAGATACGGGCACATACGGGATTCCTGCTGCCG 1096  
Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1097 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCCGCTGTCTCTAAAA 1148  
RESULT 2  
US-08-869-057-1  
; Sequence 1, Application US/08869057

; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/869,057  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P  
; AUTHORS: Henzel, William  
; AUTHORS: Dravna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
; JOURNAL: J. Biol. Chem.  
; VOLUME: 266  
; ISSUE: 32  
; PAGES: 21833-21838  
; DATE: No. 5985562 15-1991  
; US-08-869-057-1  
  
Alignment Scores:  
Pred. No.: 7,69e-225 Length: 1272  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 2 Gaps: 2  
  
US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 1 ATGAAGCTTTGCGACCTTGCAGCTCTTATCCCATTTCTCTCTCTGAGCAGCATGTC 60  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 61 TTGCGGTTTCAGAGTGGCCAAAGTTCTAGCTCTTCTAGAACCTCTAGGCAAGTTCAA 120  
Qy 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60



Db 121 GTTCTACAGAACTTACTACAAATATGAGATTGTTCTCTGCGACCGCGTAACAGCTGAC 180  
Qy 61 LeuileVallyslsLysGlnValHisPhePheValAlaSerAspValAspVal 80  
Db 181 CTTATTGTGAGAAAAAACAAGTCAATTTTGTAAATGATCTGATGTCGACATGTG 240  
Qy 81 LysAlaHisLeuAenValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 241 AAAGCCCATTTAAATGTGAGCGGAATCCATGTCAGTGTCTTGCTGGCAGAGCTGGAAGAT 300  
Qy 101 LeuileGlnGlnGlnLeSerAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 301 CTTATTCAACAGCAGATTTCCACACACACAGTCAGCCCGAGCCTCCGCATCGTACTAT 360  
Qy 121 GluGlnTyrHisSerLeuAenGluLeuTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 361 GAACAGTATCTACTTAATGAATCTATTCTTGGATAGATTTTAACTAGAGGCAT 420  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 421 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCAITTTGAGAAGTACCCCACTCTATGTT 480  
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAlaIleThrIleAspCysGlyIle 180  
Db 481 TTAAGGTTTCTGAAAAGAACAAACAGCCAAAATGCCATATGATGATGCTGTGGAATC 540  
Qy 181 HisAlaArgGluTTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197  
Db 541 CATGCCAGAAATGGATCTCTCTCGTCTTCTGCTTGTGTTTCATAGGCCATATAACTCAA 600  
Qy 197 ----- 197  
Db 601 TTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATG 660  
Qy 198 -----AnArgMetTrpArgLys 203  
Db 661 CCGGTGGTTAATGTGAGCGGTTATGACTACTCATCGGAAAAAAGAAATCGAATGTGAGAAAG 720  
Qy 204 AsnArgSerPheTyrAlaAenAsnHisCysIleGlyThrAspLeuAenSerAsnPheVal 223  
Db 721 AACGGTTCTTCTATGGACAATCATTTGATCGGAACAGACCTGGAATAGGAATTTGCT 780  
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243  
Db 781 TCCAAACACTGGTGTGAGGAAGTGATCCAGTTCTCTGCTCGGAAACCTACTGTGGA 840  
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263  
Db 841 CTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTTCTTGAGAAGAAATATC 900  
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db 901 AACCAAGTTAAGCATACATCAGATGATTCATCTATCTCCAGCATATAGTGTTCATAT 960  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303  
Db 961 TCCTATACAGAACTAAAGCAAGACCATGAGGAATGCTCTAGTAGCCAGTGAAGCA 1020  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1021 GTTCGTGCTATTGCAAAAATAGTAAATAATACCAAGGTATACATGCGCCATGGCTCAGAA 1080  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyr 343  
Db 1081 ACCTTATACCTAGCTCTCTGAGGTGGGACGATTTGGATCTATGATTTGGGCATCAATAT 1140  
Qy 344 SerPhe-----Th 346  
Db 1141 TCGTTTAACTTGAATTCGAGATACCGGCACATACCGATTCTTGCTCGCGGACGCTTAC 1200  
Qy 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1201 ATCAAAACCCACTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1243

RESULT 3  
US-07-649-591B-2  
; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: hybridization probe  
; LOCATION: 133 to 178  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: potential clip site  
; LOCATION: 380 to 382  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: signal sequence  
; LOCATION: 41 to 106  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
US-07-649-591B-2  
Alignment Scores: Pred. No.: 1,34e-224 Length: 1749  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)

Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGCAGCCTTGAGTCTTGATCCCATTTGTTCTCTGTGTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTCGGTTTACAGAGTGGCAAGTCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCAA 160  
Qy 41 ValLeuGlnAenLeuThrThrTyrGluileValLeuTrpGlnProValThrAlaAsp 60  
Db 161 GTTCTACAGAATCTTACTACAAACATATAGAGATTGTCTCTGGCCGCGTAACAGCTGAC 220  
Qy 61 LeuileValLysLysGlnValHisPheValAenAlaSerAspValAspAsnVal 80  
Db 221 CTTATTGTGAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGCAATGTG 280  
Qy 81 LysAlaHisLeuAenValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 281 AAAGCCATTTAAATGTGAGCGAATTCATGCGATGTCTTGTCTGGCAGAGCTGGAAGAT 340  
Qy 101 LeuileGlnGlnIleSerAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGCAGATTTTCAACGACACATGTCAGCCCCGAGCTCCGCATCTACTAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluileTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 401 GAAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTTATAACTGAGAGCAT 460  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCATTTGGATCTCTCAITTTGAGAAGTACCCCACTCTATGTT 520  
Qy 161 LeuLysValSerGlyLysGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIle 180  
Db 521 TTAAGGTTTTCTGAAAGAAGAACACAGCCAAAATGCCATATGGATTGACTGTGGAATC 580  
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197  
Db 581 CATGCCAGAAATGGATCTCTCTGCTTCTGCTTGTGTTGTTTCATAGGCCATATAACTCAA 640  
Qy 197 ----- 197  
Db 641 TTCTATGGGATAATAGGCAATATACCAATCTCTGAGCTTGTGGATTTCTATGTTATG 700  
Qy 198 -----AsnArgMetTrpArgLys 203  
Db 701 CCGTGGTTAATGTGGACGGTTATGACTACTCATCGGAAAAAAGAAATCGAATGTGGAGAAG 760  
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223  
Db 761 AACCGTTCTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTTGCT 820  
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243  
Db 821 TCCAAACACTGGTGTGAGGAAGTGCAATCCAGTTCCTCATGCTCGGAAACCTACTGTGA 880  
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263  
Db 881 CTTTATCTAGTCAGAACCAAGAGTAGAGGAGTGGCTAGTTCTTCTGAGAAAGAAATATC 940  
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db 941 AACCAAGATTAAGCATATACATCAGCATGCTCATCTCACTCCAGCATATAGTGTTCATAT 1000  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLysLeuSerLeuValAlaSerGluAla 303  
Db 1001 TCCTATACAGAAAGTAAAGGAAAAACCATCAGGAACCTGCTCTAGTACGCGAGTGAAGCA 1060  
Qy 304 ValArgAlaIleAspLysThrSerLysAenThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1061 GTTGTGCTATGAGAAACATAGTAAATAACAGGATATACATATGGCCATGGCTCAGAA 1120  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLysTyr 343  
Db 1121 ACCTTATACCTAGCTCCTGGAGGTGGGACGATTTGGATCTATGATTTGGGCATCAATAT 1180  
Qy 344 SerPhe-----Th 346

Db 1181 TCGTTTACAATTGAATTCGAGATACGGGCACATACGATTCCTGTGCGGAGCGTTAC 1240  
Qy 346 rSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1241 ATCAACCCACCTGTAGAGAGCTTTTG(CGCTGTCTCTTAAA 1283  
RESULT 4  
US-08-277-540-2  
; Sequence 2, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasek, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1CID1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-277-540-2  
Alignment Scores:  
Pred. No.: 1.34e-224 Length: 1749  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGACAGCCTTGACGCTCTTATCCCATTTCTTCTGTGAGACGATGTC 100  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTCGGTTTACAGAGTGGCAAGTCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCAA 160





Qy 63 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAsnValLysAla 82  
Db 148 AAACCTCACATACAGTTGACTCGGTGTAAGAGCAGAGATATTTGGCTGTGGAAGAC 207  
Qy 83 HisLeuAsnValSerGlyLysProCysSerValLeuLeuAlaAspValGluAspLeuLeu 102  
Db 208 TTTCTGGAGCAGAGTAACTCAATATAGAGTACTCAATAACACCTGAGATCTGTCTC 267  
Qy 103 GlnGlnGlnLeuSerAspThrValSerProArgAlaSerTyrTyrGluGln 122  
Db 268 GAGGCTCAGTTGACAGCAGATC-----CGTCAACTGCACACAGTATGAGAAG 318  
Qy 123 TyrHisSerLeuAsnGluLeuTyrSerTrpLeuGluPheLeuThrGluArgHisProAsp 142  
Db 319 TACAACAACCTGGGAACGATGAGGCTTGGACTAAGCAAGTCACCAAGTGAATAATCCAGAC 378  
Qy 143 MetLeuThrLysLysHisGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162  
Db 379 CTCATCTCTGCACAGCCATCGGAACACTACATTTTGGAAACAATATATACCTCTCAAG 438  
Qy 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyLysHisAla 182  
Db 439 GTT---GCAAACTGGACCAATAAGCTGCCATTTTCATGACTGTGGTTCCATGCC 495  
Qy 183 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195  
Db 496 AGAATGGATTTCCCATGCAATTTTGCAGTGGTTTGTGAGAGAGGCTGTCTCACCTAT 555  
Qy 195 ----- 195  
Db 556 GGATATGAGATCATATGACAGAAATTCCTCAAGCTAGACTTTTATGTCTTGCCTGTG 615  
Qy 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 205  
Db 616 CTCATATATTGATGCTATCATCTACCTGGACCAAGACCGAATGTGGAGAAAGACCCGC 675  
Qy 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225  
Db 676 TCTACCAATGCTGGAACCTACCTGCAATGGCACAGACCCCAACAGAAATTTT---GATGCT 732  
Qy 226 HisTrpCysGluGluGluAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245  
Db 733 GGGTGGTGCAACCTGAGAGCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGCT 792  
Qy 246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 265  
Db 793 GCAGATCTGAAAGAGACCAAGCCCTGCTGATTTTATACCAACACCTCTCTCTCC 852  
Qy 266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285  
Db 853 ATCAAGCATACCTGACGATCCATCATCTACAGATGATCTCTACCCCTTATTCCTAT 912  
Qy 286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 305  
Db 913 GATTACAACTCCCGAGAACAAATGCTGAGTGAATTAACCTGGCTAAGGCTGCGGTGAAA 972  
Qy 306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325  
Db 973 GAACCTT---GCTACACTGTATGGCACCAGTACACATACGCGCCAGAGAGCTACACAAATC 1029  
Qy 326 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyLysTyrSerPhe 345  
Db 1030 TATCTGCTGTGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAATATTCCTTC 1089  
Qy 346 Thr 346  
Db 1090 ACC 1092

## RESULT 7

US-08-860-882A-56

; Sequence 56, Application US/08860882A

; Patent No. 5985281

; GENERAL INFORMATION:

APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-PIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUM  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-56

Alignment Scores:  
Pred. No.: 1,25e-71 Length: 1263  
Score: 639.00 Matches: 135  
Percent Similarity: 53.83% Conservative: 69  
Best Local Similarity: 35.62% Mismatches: 131  
Query Match: 33.44% Indels: 44  
DB: 2 Gaps: 7

US-09-980-881A-2 (1-360) x US-08-860-882A-56 (1-1263)

Qy 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla----PheGln 24  
Db 4 CTCCTTGTTCTGTGACTGTGGCCCTGGCATCTGCTCATCATCGTGTGAGCAGCTTTGAA 63  
Qy 25 SerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44  
Db 64 GCGAGAGAGGTGTCTCGTGTAAACGTTGAAGATGAAATACATTAACATAATCCGCGAG 123  
Qy 45 LeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64  
Db 124 TTGGCCGACGACGACCCGAGATTCCTCTGGAAGCCAGATTCTGTGCACAAATCAAACT 183  
Qy 65 LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAlaHisLeu 84  
Db 184 CACAGTACAGTTGACTTCCGTGTAAAGCAGAGATACTGTCTACTGTGGAGATGTCTA 243  
Qy 85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIleGlnGln 104  
Db 244 AAGCAGATGAACCTACAATACAAGGTACTCTGATAAGCAACCTGAGAAATGTGGTGGGCT 303

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Qy 105 GlnIleSerAenAepThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db 304 CAGTTTGATGACGGGTT-----CGTCAACAGGACACAGTATGAGAGTCAAC 354
Qy 125 SerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAepMetLeu 144
Db 355 AAGTGGGAAACGATAGAGGCTTGACTCAACAGTCCGCTGAGAAATCCAGCCCTCATC 414
Qy 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164
Db 415 TCTCGCAGTGTATCGGAACACATTTGAGGACCGCTATTATCTCTCTGAAGTT--- 471
Qy 165 GlyLysGluGlnThrAlaLysAenAlaIleTrpIleAepCysGlyIleHisAlaArgGlu 184
Db 472 GGCAGAGTGGACAAAATAAGCTGCCATTTTCATGAGCTGTGTGTTTCCATGCCAGAG 531
Qy 185 TrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 532 TGGATTCTCTCGCATCTCGCAGTGGTTTGTAAAGAGAGGCTGTCTACTATGGACGT 591
Qy 195 ----- 195
Db 592 GAGATCCAGTGCAGAGCTTCTCGCAAGTTAGACTTTTATGTCCTGCTGCTCAAT 651
Qy 196 -----GlyHis-----AenArgMetTrpArgLysAenArgSerPhe 207
Db 652 ATTGATGCTACTATCTACCTCGGACCAAGACCGGATTTTGGAGAAAGACTCGCTCCACC 711
Qy 208 TyrAlaAenAenHisCysIleGlyThrAspLeuAenSerAenPheValSerLysHisTrp 227
Db 712 CATACTGATCTAGCTGATTTGGCAGACAGCCCAACAGAAATTTT---GATGCTGGTTGG 768
Qy 228 CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db 769 TGTGAATTTGAGCGCTCTCGAAACCCCTGTGATGAACTTACTGTGGACCTGCCGCGAG 828
Qy 248 SerGluProGluValLysAlaValAlaSerPheLeuArgAenIleAenGlnIleLys 267
Db 829 TCTGAAAGGAGACCAAGCGCTGGCTGATTTCAATCCGCAACAACTCTCTTCCATCAAG 888
Qy 268 AlaTrpIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArg 287
Db 889 GCATATCTGCAATCCACTCTGATCTCCCAATGATGATCTACCTTACTCATATGCTTAC 948
Qy 288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
Db 949 AAACCTCGTGAGAACAAATGCTGAGTTGAATGCCCTGCTAAAGCTACTGTGAAAGAACTT 1008
Qy 308 AspLysThrSerLysAenThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
Db 1009 ---GCCTCAGTCGACGGCACCAGTACATATATGCGCGGAGGTACAAACATCTATCCT 1065
Qy 328 AlaProGlyGlyAspAspTrpIleTyrAspLeuGlyLysTyrSerPheThr 346
Db 1066 CTGCTGGGGGCTCTGACACTGGCTTATGACCAAGGATCAGATATCTCTTCCACC 1122
```

## RESULT 8

US-09-011-769A-38

; Sequence 38, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; BLAKEY, David C.

; DAVIES, David H.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison &amp; Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-10S

SOFTWARE: MS word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011-769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612245.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1263 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-011-769A-38

## Alignment Scores:

Pred. No.:	1,25e-71	Length:	1263
Score:	639.00	Matches:	135
Percent Similarity:	53.83%	Conservative:	69
Best Local Similarity:	35.62%	Mismatches:	131
Query Match:	33.44%	Indels:	44
DB:	4	Gaps:	7

US-09-980-881A-2 (1-360) x US-09-011-769A-38 (1-1263)

Qy 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24

Db 4 CTCTTGTTCTGTGACTGTGGCCCTGGCATCTGCTCATCTGCTGCTGAGTGGTGGACCTTTGAA 63

Qy 25 SerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44

Db 64 GCGCAGAGAGTGTTCGGTGTAAAGTGAAGATGAAATACATTAACATAATCCGCGAG 123

Qy 45 LeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64

Db 124 TTGCCACGACGACGCCAGATTTGACTTCTTGAAGCCAGATTCTGTCTCACACAAATCAACCT 183

Qy 65 LysLysGlnValHisPhePheValAenAlaSerAspValAspAsnValLysAlaHisLeu 84

Db 184 CACAGTACAGTTCAGTTCCTGTTAAACGACAGAGATCTGCTCACTGTGGAGATGTTCTA 243

Qy 85 AsnValSerGlyIleProCysSerValIleLeuAlaAspValGluAspLeuIleGlnGln 104

Db 244 AAGCAGATCACTACATAACAGGTACTGATAAGCAACCTGAGAAATGTGGTGGAGGCT 303

Qy 105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124

Db 304 CAGTTTGATGCGGGTT-----CGTCAACAGGACACAGTATGAGAGTCAAC 354

Qy 125 SerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAepMetLeu 144

Db 355 AAGTGGGAAACGATAGAGGCTTGACTCAACAGTCCGCTGAGAAATCCAGCCCTCATC 414

Qy 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValSer 164

Db 415 TCTCGAGTGTATCGGAACACACATTTGAGGAGCGGCTATTATTACCTCTCTGAAGTT--- 471  
Qy GlyLysGluGlnThrAlaLysAsnAlaIleTyrPheLeuAspCysGlyIleHisAlaArgGlu 184  
Db 472 GGCAAGCTGGACAAATAAGCCTGCCATTTTCATGACTGTGGTTCCATGCCAGAGAG 531  
Qy TrpIleSerProAlaPheCysLeuTyrPheIle----- 195  
Db 532 TGGATTTCTCTGCAATTCGCAGTGGTTCGTAAGAGAGAGGCTGTTCGTACCTATGGAGCT 591  
Qy 195 ----- 195  
Db 592 GAGATCCAAAGTGACAGAGCTTCTCGCAAGTTAGACTTTTAATGCTCCCTGCTCAAT 651  
Qy 196 -----GlyHis-----AsnArgMetTyrArgLysAsnArgSerPhe 207  
Db 652 ATTGATGGCTACATCTACACCTGGACCCAGAGCGGATTTGGAGAAAGACTCGCTCCACC 711  
Qy TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLysHisTyr 227  
Db 712 CATACTGATCTAGCTGATGGCACACAGCCCAACACAGAAATTTT---GATGCTGCTGG 768  
Qy CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247  
Db 769 TGTGAATTTGAGGCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCCGCAGAG 828  
Qy SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267  
Db 829 TCTGAAAGGAAACCAAGGCGCTGGTGTTCATCCGCAACAAACTCTCTCCATCAAG 888  
Qy AlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArg 287  
Db 889 GCATATCTGCAATCCACTCTGCTCCAAATGATGATACCTTACTCATATGCTTAC 948  
Qy SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307  
Db 949 AAATCGGTGAGAACAAATGCTGAGTTGAATGCCCTGCTAAAGCTACTGTGAAAGAACTT 1008  
Qy AspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327  
Db 1009 ---GCCTACTGCGACGCGCACCAAGTACATATGCGCGGAGCTACACAACTCTATCCT 1065  
Qy AlaProGlyGlyAspAspTyrPheTyrAspLeuGlyIleLysTyrSerPheThr 346  
Db 1066 GCTGCTGGGGCTCTGACAGCTGGGCTTATGACCAAGGAATCAGATATTCCTTCACC 1122

## RESULT 9

US-08-860-882A-71  
; Sequence 71, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGLESE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-PIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1284 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-860-882A-71

Alignment Scores:  
Pred. No.: 1,18e-70 Length: 1284  
Score: 631.50 Matches: 129  
Percent Similarity: 54.57% Conservative: 68  
Best Local Similarity: 35.73% Mismatches: 121  
Query Match: 33.05% Indels: 43  
Gaps: 6

US-09-980-881A-2 (1-360) x US-08-860-882A-71 (1-1284)

Qy 23 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 42  
Db 85 TTTGAAAGCGGAGAGGTTCCTGTTAAGCTTGAAGATGAAATACATTAAACATAATC 144  
Qy 43 GlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 62  
Db 145 CGCGAGTTGGCCAGCAGCCAGATTCCTCTGGAGCCAGATTCCTGCACACAATC 204  
Qy 63 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 82  
Db 205 AAACCTCAGTACAGTTGACTTCCGTGTTAAAGCAGAGATACTGCTACTGTGGAGAT 264  
Qy 83 HisLeuAsnValSerGlyIleProCysSerValLeuAlaAspValGluAspLeuIle 102  
Db 265 GTTCTAAAGCAGAAATGAATCAACATCAAGGTACTGATAAGCAACCTGAGAAATGGTG 324  
Qy 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122  
Db 325 GAGGCTCAGTTTATAGTAGCGGGTT-----CGTGCAACAGGACACAGTTATGAGAAG 375  
Qy 123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142  
Db 376 TACACAAGTGGGAAACGATAGAGCTTGAGCTTCAACAAGTCCCACTGAGAAATCCAGCC 435  
Qy 143 MetLeuThrLysIleHisIleGlySerSerPheGlyLysTyrProLeuTyrValLeuLys 162  
Db 436 CTCATCTCTGCGAGTGTATTGCGAACCAACATTTTGGGAGCGCGCTATTACCTCCCTGAAG 495  
Qy 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyIleHisAla 182  
Db 496 GTT---GGCAAGCTGGACAAAATAAGCTGCCATTTTCATGAGCTGTGGTTCCATGCC 552  
Qy 183 ArgGluTrpIleSerProAlaPheCysLeuTyrPheIle----- 195  
Db 553 AGAGAGTGGATTTCTCTGCAATTCCTCCAGTGGTTTGAAGAGAGGCTGTTCGTCTACTAT 612  
Qy 195 ----- 195  
Db 613 GGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAAGATTAGACTTTTATGTCTCGCTGTG 672  
Qy 196 -----GlyHis-----AsnArgMetTyrArgLysAsnArg 205



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Db 673 CTCATATTGATGCTACATCTACACCTGGACCAAGCCGATTTTGGAGAAAGACTCGC 732
      :::::
Qy 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
      :::::
Db 733 TCCACCCATCTAGTCTAGCTGCTGGACAGACCCCAACAGAAATTTT--GATGCT 789
      :::::
Qy 226 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245
      :::::
Db 790 GGTGGTGTGAATTGGAGCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 849
      :::::
Qy 246 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgAsnIleAsnGln 265
      :::::
Db 850 GCAGAGCTGAAGAGAGACCAAGCCCTGCTGATTTTCACCGCAACAACTCTCTCC 909
      :::::
Qy 266 IleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285
      :::::
Db 910 ATCAAGGCATATCTGACAACTCACTGCTACTCCCAAAATGATGATCTACCTTACTCATAT 969
      :::::
Qy 286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 305
      :::::
Db 970 GCTTACAACTCGGTGAGAAACAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029
      :::::
Qy 306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325
      :::::
Db 1030 GAACCT---GCTACTACGACGACCAAGTACATATGSCCGGAGCTACACAAATC 1086
      :::::
Qy 326 TyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345
      :::::
Db 1087 TATCTGCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146
      :::::
Qy 346 Thr 346
      |||
Db 1147 ACC 1149
```

## RESULT 10

```
US-09-011-769A-55
; Sequence 55, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
;           BLAKEY, David C.
;           DAVIES, David H.
;           HENNAM, John F.
;           HENNEQUIN, Laurent F.A.
;           MARSHAM, Peter R.
;           DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pillsbury Madison & Sutro, LLP
;   STREET: 1100 New York Ave., N.W.
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 1.44 Mb disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/011,769A
;   FILING DATE: 13-Feb-1998
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB96/01975
;   FILING DATE: 13-AUG-1996
;   APPLICATION NUMBER: GB 9612295.7
;   FILING DATE: 12-JUN-1996
;   APPLICATION NUMBER: GB 9611019.2
;   FILING DATE: 25-MAY-1996
;   APPLICATION NUMBER: GB 9516810.0
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; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1284 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1272
; FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: 352..1272
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-55

Alignment Scores:
Pred. No.: 1..186-70 Length: 1284
Score: 631.50 Matches: 129
Percent Similarity: 54.57% Conservative: 68
Best Local Similarity: 35.73% Mismatches: 121
Query Match: 33.05% Indels: 43
DB: 4 Gaps: 6

US-09-980-881A-2 (1-360) x US-09-011-769A-55 (1-1284)

Qy 23 PheGlnSerGlyGlnValValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 42
      |||:::
Db 85 TTTGAAGCGGAGAGAGGTGTTCCCGTTTAAGATGAAATACATAATC 144
      :::::
Qy 43 GlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 62
      :::::
Db 145 CGCGAGTTGGCCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTACACAAATC 204
      :::::
Qy 63 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 82
      |||:::
Db 205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAGATGCTGCTGTTGGAGAAT 264
      :::::
Qy 83 HisLeuAsnValSerGlyIleProCysSurValLeuLeuAlaAspValGluAspLeuIle 102
      |||:::
Db 265 GTTCTAAAGCAGAGTAACATACAAATACAGGTGCTGATAAGCAACCTGAGAAATGTGGTG 324
      :::::
Qy 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122
      :::::
Db 325 GAGCTCAGTTTGATGACCGGGTT-----CGTCAACAGGACACACAGTTATGAGAAG 375
      :::::
Qy 123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142
      |||:::
Db 376 TACAACAAGTGGGAAACGATAGAGGCTTACCTCAACAAGTCGCACTGAGAAATCCAGCC 435
      :::::
Qy 143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162
      |||:::
Db 436 CTCATCTCTGCGAGTGTATTTCGGAACCAATATTTGAGGGACGCGCTATTATACCTCCTGAAG 495
      :::::
Qy 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
      |||:::
Db 496 GTT---GGCAAGCTGGCAAAAATAAGCTTGCCATTTTCATGAGCTGTGTTTCCATGCC 552
      :::::
Qy 183 ArgGluTrpIleSerProAlaPheCysLauTrpPheIle----- 195
      |||:::
Db 553 AGAGAGTGGATTTCTCTCGCATCTTCGCACTTCGCACTGCTGCTGTTGTAAGAGAGGCTGTTCGTACCTAT 612
      :::::
Qy 195 ----- 195
      |||:::
Db 613 GGACGTGAGATCCAAGTGACAGAGCTTCACCAAGTTAGACTTTTATGCTCGCTCGCTGTG 672
      :::::
Qy 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 205
      |||:::
Db 673 CTCATATTGATGCTGCTACATCTACACCTGCACCAAGAGCCGATTTGGAGAAAGACTCGC 732
      :::::
Qy 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
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Db 733 TCCACCCATCTGGATCTAGCTGCTGGCAGACAGACCCCAACAGAAATTTT---GATGCT 789
Qy 226 HistpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 245
Db 790 GGTGGTGTGAATGAGGCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 849
Qy 246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 265
Db 850 GCAGAGTCTGAAAGGAGACCAAGGCCCTGCTGATTTTCGCGCAACAAACTCTCTCC 909
Qy 266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285
Db 910 ATCAAGGCATATCTGACAACTCCATCTGCTACTCCCAATGATGATCTACCTTACTCAT 969
Qy 286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaLaserGluAlaValArg 305
Db 970 GCTTACAACTCGGTGAGAACATGCTGAGTTGATGCCCTGGCTAAAGCTACTGTGAAA 1029
Qy 306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325
Db 1030 GAACCT---GCCCTACTGACCGCACCAAGTACACATATGGCCCGGAGCTACAAACAATC 1086
Qy 326 TyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe 345
Db 1087 TATCTGCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146
Qy 346 Thr 346
Db 1147 ACC 1149

RESULT 11
US-09-171-945-124
; Sequence 124, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEAs, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEAs
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-124

Alignment Scores:
Pred. No.: 3 59e-69 Length: 2154
Score: 623.00 Matches: 132
Percent Similarity: 53.40% Conservative: 72
Best Local Similarity: 34.55% Mismatches: 134
Query Match: 32.60% Indels: 44
DB: 3 Gaps: 7

US-09-980-881a-2 (1-360) x US-09-171-945-124 (1-2154)

Qy 3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
Db 1 ATGTGGCAGCTCTTGGTCTGCTGAGCTGTGGCCCTGGCATCTGCTCATCATGGTGGTGGAG 60
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Qy 23 ---PheGlnSerGlyGlnValValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
Db 61 CACTTTGAAGGCGAGAGAGGTGTCCGCTTAACGTTGAAGATGAAATACATTAACATA 120
Qy 42 LeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeu 61
Db 121 ATCCGCGAGTGTGGCCAGCAGCCAGATTTGACTTCTGGAAGCCAGATTCTGTGCACACAA 180
Qy 62 IleValLysLysGlnValHisPheValAsnAlaSerAspValaAspAsnValLys 81
Db 181 ATCAAACTCAGACAGTACAGTTGACTTCCGTTGTTAAAGCAGAGATACTGTCACTGTGGAG 240
Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
Db 241 AATGTTCTAAAGCAGAGATGAACTACAAATACAAGTACTGATAAGCAACCTGAGAAATGTG 300
Qy 102 IleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
Db 301 GTGGAGGCTCAGTTGATAGCCGGT---CGTGCAACAGGACACAGTTATGAG 351
Qy 122 GlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisPro 141
Db 352 AAGTACAACAGTGGGAAACGATAGAGGCTTGACTCAACAGTCCCACTGAGATCCA 411
Qy 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
Db 412 GCCCTCATCTCGCAGTGTATTATCGGAACACATTTGAGGAGCGCGCTATTACCTCTG 471
Qy 162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleThrIleAspCysGlyIleHis 181
Db 472 AAGGTT---GGCAAGCTGGACAAATAAGCCCTGCCATTTTCATGACTGTGGTTTCCAT 528
Qy 182 AlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 195
Db 529 GCCAGAGAGTGGATTTCTCTGCATTTCTGCAGTGGTTTGTAGAGAGGCTGTTCGTACC 598
Qy 195 ----- 195
Db 589 TATGGAGCTGAGATCCAAAGTGACAGAGCTTCTCGCAAGTTAGACTTTTATGTCTGCCT 648
Qy 196 -----GlyHis-----AsnArgMetTyrArgLysAsn 204
Db 649 GTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGCGCGATTTTGGAGAAAGACT 708
Qy 205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224
Db 709 CGCTCCACCATCTACTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 765
Qy 225 LysHisTyrCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 244
Db 766 GCTGGTGTGTGAATTTGGAGGCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCT 825
Qy 245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264
Db 826 GCGCAGAGTCTGAAAGGAGACCAAGGCCCTGGCTGATTTTCATCCGCAACAAACTCTCT 885
Qy 265 GlnIleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284
Db 886 TCCATCAAGGCATATCTGACATCCACTCGTACTCCCAATGATGATGATGATGATGATGAT 945
Qy 285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
Db 946 TATGCTTACAAACTCGGTGAGAACAAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTG 1005
Qy 305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324
Db 1006 AAAGAACTT---GCCTCACTGCGACGCGACCAAGTACATACATATGCGCGGAGGTACAACA 1062
Qy 325 LeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSer 344
Db 1063 ATCTATCTCTCTGCTGGGACTTCTAAAGACTGGGCTTTATGACCAAGGAATCAGATATTC 1122
Qy 345 PheThr 346
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Best Local Similarity: 33.81%      Mismatches: 135
Query Match: 32.00%      Indels: 72
DB: 4      Gaps: 11

US-09-980-881A-2 (1-360) x US-10-200-344-9 (1-1311)

Qy 1 MetLysLeuCys-----SerLeuAlaValLeuValProLleValLeuPheCysGluGln 18
Db 43 CTGGCTCTTTGCTGGCTCTTTTGAAGATCTCGAACCG-----GGGCACAGC 90

Qy 19 HisValPhe-----AlaPheGlnSerGlyGlnValLeuAlaLaLeuProArgThrSer 36
Db 91 CACCTTTATACAAACCGTCGCTGGTGATAAAGTGATAGATTATTATCCCAAAACGAA 150

Qy 37 ArgGlnValGlnValLeuGlnAsnLeuThrThrThrTyrGluLleValLeuTyrGlnPro 56
Db 151 GAGGAAGCATATGCACCTGAAGAAATATCTCATCAACTTAAGGTGGACCTGTGGCAGCC 210

Qy 57 ValThrAlaAspLeuLleValLys-----LysLysGlnValHisPheValAsnAla 74
Db 211 AGCAGTATCTCTATGATACAGAGGACAGTTACTGATGTCATATCCCCAAAATGGT 270

Qy 75 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyLleProCysSerValLeu 94
Db 271 TCCCGAGCC-----CTGTTAGCCTTCTTACAGGAAGCCAAACATCCAGTAGCAAGTCTC 324

Qy 95 LeuAlaAspValGluAspLeuLleGlnGlnLeuSerAsnAspThrValSerProArg 114
Db 325 ATAGAAGATCTTCAGAAACACACTCGAGAAGGAAGCAGCTTGACACACCCAGAGAAACCGA 384

Qy 115 AlaSerAlaSer-----TyrTyrGluGlnTyrHisSerLeuAsnGluLleTyrSerTyr 132
Db 385 AGATCCCTCTCTGATATATATGAGTTATACCTCTTACAGAAATTCAAAATGG 444

Qy 133 IlegluPheLleThrGluArgHisProAspMetLeuThrLysLleHisLleGlySerSer 152
Db 445 ATGCATCATCTGAATAAACTCACTCAGGCCTCATCTCACATGTTCTCTATTGGAAGATCA 504

Qy 153 PheGluLysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsn 172
Db 505 TATGAGGAAGATCTCTTTTATTATTAAGCTG---GGCAGACATCACGACTCAAAAGA 561

Qy 173 AlaLleTrpLleAspCysGlyLleHisAlaArgGluTrpLleSerProAlaPheCysLeu 192
Db 562 GCTGTTGGTAGACTGTGTTATTCATGCAAGAAATGGATTGCTCTGCTTGTTCAG 621

Qy 193 TrpPheLle----- 195
Db 622 TGGTTTGTAAAAAGAGCTCTTCTAATATATAAGAGTGAGCCAGCCATGAGAAAAATGTTG 681

Qy 195 ----- 195
Db 682 AATCATCTATATTTCTATATCATGCTGTTTAAACGTCGATGGATACCACTTTTAGTTGG 741

Qy 196 GlyHisAsnArgMetTrpAtqLysAsnArgSerPheTyrAlaAsnAsnHisCysLleGly 215
Db 742 ACCAATGATCAATTTTGGAGAAAACAGAGTCAGGAACCTCAAGTTTCGTCGCCGTGGA 801

Qy 216 ThrAspLeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSer 235
Db 802 GTGGATGCCAATAAGAACTGGAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCAC 858

Qy 236 SerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaVal 255
Db 859 CCTTGTGATGACATACTGTGGCCCTTTTCCAGAATCTGAGCCGGAAGTGAAGCGCTGTA 918

Qy 256 AlaSerPheLeuArgArgAsnLleAsnGlnLleLysAlaTyrLleSerMetHisSerTyr 275
Db 919 GCTAACTTCTTCGAAACACAGAAACACATTAGGGCTTATCTCTCTTTCATGCATAT 978

Qy 276 SerGlnHisLleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlu 295
Db 979 GCTCAGATGTTACTGTATCCCTATTCTTACAAATATGCAAAATATCCCAATTTTAGATGT 1038
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296 LeuSerLeuValAlaSerGluAlaValAaGAlaIleAspLysThrSerLysAsnThrArg 315
Db 1039 GTGGAATCTGCAGCTTATAAAGCTGTGAATGCACCT---CAGTCAGTATACGGGGTACGA 1095

Qy 316 TyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyr 335
Db 1096 TACAGATATGAGCAGCCTCCACACGTTGATGTGAGCTCTGTAGCTCAATGGATTGG 1155

Qy 336 IleTyrAspLeuGlyLleLysTyrSerPhe----- 345
Db 1156 GCCTACAAAATGGAATACCTTATGCATTCGTTTCGAACTAGCTGACACTGGGATATTT 1215

Qy 346 -----ThrSerIleProValGluLysLeu 354
Db 1216 GGATTTTACTCCAGAGATGCTCATCAAAACCCACCTGTACAGAAACTA 1264

RESULT 15
US-08-782-760-5
; Sequence 5: Application US/08782760
; Patent No. 5948668
; GENERAL INFORMATION:
; APPLICANT: Hartman, Jacob
; APPLICANT: Fulga, Netta
; APPLICANT: Mendelovitch, Simona
; APPLICANT: Gorecki, Marian
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIORITY DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; US-08-782-760-5

Alignment Scores: 2.28e-67 Length: 927
Pred. No.: 604.00 Matches: 125
Score: 60.14% Conservative: 44
Percent Similarity:
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Best Local Similarity: 44.48% Mismatches: 72
Query Match: 31.61% Indels: 41
DB: 2 Gaps: 5

US-09-980-881A-2 (1-360) x US-08-782-760-5 (1-927)

Qy 115 AlaSerAlaSerTyTyTyGluGluHisSerLeuAsnGluIleTySerTrpIleGlu 134
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    |||||

Qy 135 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 154
    ::|||
Db 61 CAAGTTGCCACTGATAATCCAGACCTTGTCACTCAGAGCGTCATTGCAACCAATTGAA 120
    ::|||

Qy 155 LysTyProLeuTyValLeuValSerGlyLysGluGlnThrAlaLysAsnAlaIle 174
    ::|||
Db 121 GGAGTAACTGATGTCCTCAAGATT--GGTAAACTAGACCGAATAAGCCTGCCATC 177
    ::|||

Qy 175 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 194
    ::|||
Db 178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTCTCTCGCATTCCTGTCAGTGGTTT 237
    ::|||

Qy 195 Ile----- 195
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Db 238 GTGAGAGAGGCTGCCGTACCTATATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297
    ::|

Qy 196 -----GlyHis----- 197
    ::|

Db 298 CTGGATTTCATGTTCTGCCCTGGTCAACATTGATGGCTATGTCTACACTGGACTAAG 357
    ::|||

Qy 198 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 217
    ::|||
Db 358 GACAGAATGTGGAAAAACCCGCTCTACTATGGCTGGAAAGTCTCTGCTGGGTGGTAGAC 417
    ::|||

Qy 218 LeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 237
    |||||
Db 418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGAGCTTCTCGAGTCCCTGC 474
    |||||

Qy 238 SerGluThrTyTyCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSer 257
    |||||
Db 475 TCTGAAACTTACTGTGGACAGCCCGCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534
    |||||

Qy 258 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGln 277
    |||||
Db 535 TTATCCGCAACAACCTCTCCACCATCAGCCCTACTGACCATCCACTCATCTACTACAG 594
    |||||

Qy 278 HisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluLeuSer 297
    ::|||
Db 595 ATGATGCTCTACCTTACTCTCTATGACTACAAACTGCTGAGAACTATGAGGAATTGAAT 654
    ::|||

Qy 298 LeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyThr 317
    ::|||
Db 655 GCCCTGTGTAAGGTGGCGCAAGAGAGCTT---GCCACTCTGCATGGCCACCAAGTACACA 711
    ::|||

Qy 318 HisGlyHisGlySerGluThrLeuAlaProGlyGlyGlyAspAspTrpIleTy 337
    ::|||
Db 712 TATGGCCAGAGAGCTACAACTATCTCTGCTGCTGGGGATCTGACGACTGCTCTTAT 771
    ::|||

Qy 338 AspLeuGlyIleLysTySerPheThrSerAsnProValGluLysLeuLeuProLeu 357
    |||||
Db 772 GATCAGGGAATCAATATTCTTTACCTTTGAACT--CCGGGATACAGGCTTCTTTGGCTT 830
    |||||

Qy 358 Ser 358
    |||
Db 831 TCT 833
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Job time : 118.873 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 626.949 Seconds  
(without alignments)  
2944.316 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=ext -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0  
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- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq\*
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- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq\*
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- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Alignment Scores:

Result No.	Score	Query Match	Length	DB ID	Description
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2	1849.5	96.8	1625	14	US-10-212-877-1
3	1832	95.9	1728	9	US-09-880-107-2396
4	1808.5	94.6	1344	16	US-10-115-479-69
5	1808.5	94.6	1743	16	US-10-115-479-67
6	1729	90.5	1272	15	US-10-379-836-1
7	1439.5	75.3	1037	16	US-10-115-479-63
8	1393.5	72.9	1132	16	US-10-115-479-65
9	889	46.5	1400	9	US-09-925-302-24
10	889	46.5	1400	10	US-09-925-302-24
11	623	32.6	2154	9	US-09-910-059-124
12	621.5	32.5	1332	9	US-09-954-456-1141
13	620.5	32.5	1633	15	US-10-341-434-187
14	620.5	32.5	1740	14	US-10-116-802-95
15	619.5	32.4	1254	14	US-10-223-546-3
16	619.5	32.4	1622	14	US-10-429-546-1
17	619.5	32.4	1622	15	US-10-429-802-21
18	619.5	32.4	1622	16	US-10-430-503-12
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21	611.5	32.0	1302	17	US-10-477-515-1
22	611.5	32.0	1311	13	US-10-200-344-9
23	611.5	32.0	1993	15	US-10-274-639-33
24	611.5	32.0	1993	16	US-10-333-574-33
25	609.5	31.9	1907	18	US-10-757-262-127
26	591	30.9	416	9	US-09-960-352-14595
27	564	29.5	2128	13	US-10-200-344-13
28	563	29.5	1125	9	US-09-888-615-2
29	563	29.5	1332	15	US-10-176-306-75
30	563	29.5	1603	15	US-10-176-306-73
31	556	29.1	1826	15	US-10-252-157-453
32	546	28.6	1200	14	US-10-200-910-7
33	546	28.6	1200	18	US-10-843-130-7
34	543	28.4	1870	9	US-09-910-059-112
35	543	28.4	1870	17	US-10-608-710-3
36	528.5	27.7	1050	13	US-10-200-344-11
37	527.5	27.6	991	16	US-10-383-201-93
38	519.5	27.2	1260	16	US-10-257-174-16
39	519.5	27.2	1311	14	US-10-200-910-5
40	519.5	27.2	1311	16	US-10-257-174-15
41	519.5	27.2	1311	17	US-10-451-821-1
42	519.5	27.2	1311	18	US-10-843-130-5
43	519.5	27.2	1348	16	US-10-072-012-315
44	519.5	27.2	1641	17	US-10-381-820A-5
45	514.5	26.9	1295	17	US-10-363-829-148

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

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Pred. No.: 4,27e-219 Length: 1625
Score: 1849.50 Matches: 355
Percent Similarity: 94.18% Conservative: 1
Best Local Similarity: 93.92% Mismatches: 4
Query Match: 96.78% Indels: 18
DB: 9 Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy 1 MetLysLeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 17 ATGAAGCTTTGCAGCTTCCTGATCCCACTTTCTCTCTGAGCAGCATGTC 76
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 77 TTCGCGTTTCAGAGTGCCCAAGTCTAGCTCTTCTAGAACCTCTAGGCAAGTTCAA 136
Qy 41 ValLeuGlnLeuThrThrThrGluLeuValLeuTyrGlnProValThrAlaAsp 60
Db 137 GTTCTACAGATCTTACTACACATATGATGTTCTCTGGCAGCGGTACAGCTGAC 196
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80
Db 197 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG 256
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATGACGATGTTCTGTCGAGATGTGGAAGAT 316
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyr 120
Db 317 CTTATTCAACAGCAGATTTCCAAAGACACAGTACGCCCGGAGCTCCGCATCGTACTAT 376
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 436
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 437 CCTGATATGCTTACAAAAATCCATTTGGATTCCTCAATTTGAGAAAGTACCCACTCTATGTT 496
Qy 161 LeuLysValSerGlyLysGluThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 497 TTAAGGTTTCTGAAAGAAACAAGCAGCCAAAATGCCATATGATGATGTGGAAATC 556
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
Db 557 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 616
Qy 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
Db 617 TGGAGAAAGAACCGTTCTTCTATCGCAACAATCAATTCGATCGGAACAGACCTGAAATAGG 676
Qy 221 AsnPheValSerLysHisTrpCysGluGluGluAlaSerSerSerSerCysSerGluThr 240
Db 677 AACTTTGCTTCCAAACACTGGTGTGAGAGAGTGCATCCAGTTCTCTATGCTCGGAACCC 736
Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
Db 737 TACTGTGAGCTTTATCTGAGTCAAGAACCAAGTGAAGGAGTGGCTAGTTCTTCTGAGA 796
Qy 261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
Db 797 AGAAATATCAACAGATTAAGACATATCATGACATGCAATTCATATCATCTCCAGCATATAGT 856
Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
Db 857 TTTCATATTCCTATACAGAAAGTAAAGCAAGCAACCAATGAGGAACTGTCTCTAGTAGCC 916
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
Db 917 AGTGAAGCAGTTCGTGCTATTGAGAAAAATAGTAAAAAATACACAGGTATACACATGGCCAT 976
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321 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 340
977 GGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCATGTATGATTTGGGC 1036
341 IleLysTyrSerPhe----- 345
1037 ATCAATATTCGTTTACATTTGAATTCGAGATACGGGCACATACGATTTCTTGCTGCCG 1096
346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
1097 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGCTGTCTCTAAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores:
Pred. No.: 4,27e-219 Length: 1625
Score: 1849.50 Matches: 355
Percent Similarity: 94.18% Conservative: 1
Best Local Similarity: 93.92% Mismatches: 4
Query Match: 96.78% Indels: 18
DB: 14 Gaps: 1

US-09-980-881A-2 (1-360) x US-10-212-877-1 (1-1625)

Qy 1 MetLysLeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 17 ATGAAGCTTTGCAGCTTCCTGATCCCTTGTACCCATTTCTCTCTGAGCAGCATGTC 76
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 77 TTCGCGTTTCAGAGTGCCCAAGTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 136
Qy 41 ValLeuGlnLeuThrThrThrGluLeuValLeuTyrGlnProValThrAlaAsp 60
Db 137 GTTCTACAGATCTTACTACACATATGATGTTCTCTGGCAGCGGTACAGCTGAC 196
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80
Db 197 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG 256
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATGACGATGTTCTGTCGAGATGTGGAAGAT 316
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyr 120
Db 317 CTTATTCAACAGCAGATTTCCAAAGACACAGTACGCCCGGAGCTCCGCATCGTACTAT 376
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGCAT 436
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 437 CCTGATATGCTTACAAAAATCCATTTGGATTCCTCAATTTGAGAAAGTACCCACTCTATGTT 496
Qy 161 LeuLysValSerGlyLysGluThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 497 TTAAGGTTTCTGAAAGAAACAAGCAGCCAAAATGCCATATGATGATGTGGAAATC 556
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
Db 557 CATGCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 616
Qy 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
Db 617 TGGAGAAAGAACCGTTCTTCTATCGCAACAATCAATTCGATCGGAACAGACCTGAAATAGG 676
Qy 221 AsnPheValSerLysHisTrpCysGluGluGluAlaSerSerSerSerCysSerGluThr 240
Db 677 AACTTTGCTTCCAAACACTGGTGTGAGAGAGTGCATCCAGTTCTCTATGCTCGGAACCC 736
Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
Db 737 TACTGTGAGCTTTATCTGAGTCAAGAACCAAGTGAAGGAGTGGCTAGTTCTTCTGAGA 796
Qy 261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
Db 797 AGAAATATCAACAGATTAAGACATATCATGACATGCAATTCATATCATCTCCAGCATATAGT 856
Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
Db 857 TTTCATATTCCTATACAGAAAGTAAAGCAAGCAACCAATGAGGAACTGTCTCTAGTAGCC 916
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
Db 917 AGTGAAGCAGTTCGTGCTATTGAGAAAAATAGTAAAAAATACACAGGTATACACATGGCCAT 976
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Db 437 CCTGATATGCTTACAAAAATCCATTTGGATGCTCTATTTGAGAAAGTACCCACTCTATGTT 496  
Qy 161 LeuLysValSerGlyLysGluThrAlaLysAsnAlaIleTrpIleAspCysGlyLe 180  
Db 497 TTAAGGTTTCTGAAAGAACCAAGACGCCAAAATGCCATATGATGGATTGACTGTGGAATC 556  
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
Db 557 CATGCCAGAGAAATGATCTCTCTGCTTCTTGCTTGTGGTTTCATAGGCCATATCGAATG 616  
Qy 201 TrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220  
Db 617 TGGAGAAAGAACCGTTCTTTCTATCGCAACAATCATTTGCATCGGAACAGACCTGAATAGG 676  
Qy 221 AsnPheValSerLysHisTrpCysGluGluClyAlaSerSerSerCysSerGluThr 240  
Db 677 AACTTTTGCTTCCAAACACTGGTGTGAGAAAGTGCATCCAGTTCCCTCATGCTCGGAACC 736  
Qy 241 TyrCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Db 737 TACTGTGAGCTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGA 796  
Qy 261 ArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHisIleVal 280  
Db 797 AGAAATATCAACCAAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 856  
Qy 281 PheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
Db 857 TTTCCATATTCCTATACACGAAAGTAAAGACCAAGACCATGAGGAACCTGTCTAGTAGCC 916  
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyThrHisGlyHis 320  
Db 917 AGTGAGCAGTTCTGCTATTGAGAAATTTAGTAAATAATACCAGGTATACATGCGCAT 976  
Qy 321 GlySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTyAspLeuGly 340  
Db 977 GGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTCGATCTATGATTTGGGC 1036  
Qy 341 IleLysTySerPhe----- 345  
Db 1037 ATCAAAATATTCGTTTACAAATTTGAACCTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 1096  
Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1097 GAGCGTTACATCAAAACCCCTGTAGAGAGCTTTTGGCGGTCTCTCTAANA 1148

RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:

Pred. No.: 7,12e-217 Length: 1728  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservatives: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 9 Gaps: 2

US-09-980-881A-2 (1-360) x US-09-880-107-2396 (1-1728)

Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 20 ATGAAGCTTTGACAGCCTTGAGTCCCTTGATACCCATTGTTCTCTCTGTCGACGACGATGC 79  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 80 TTCGCGCTTTCAGAGTGGCAAGTTCCTAGCTGCTCTTCTAGAACCTCTTAGGCAAGTTCAA 139  
Qy 41 ValLeuGlnAsnLeuThrThrTyGlyIleValLeuTrpGlnProValThrAlaAsp 60  
Db 140 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 199  
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80  
Db 200 CTTATTGTGAAGAAAAACAAGTCCATTTTTTGTAAATGCATCTCATGTCGACAATGTG 259  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 260 AAAGCCCATTTAAATGTGAGCGGAATTCATATGAGTGTCTTGTGGCAGACGTGGAAGAT 319  
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyTy 120  
Db 320 CTTATTTCACAGCAGATTTCCACGACACAGTCAGCCCCCGAGCCTCCGATCGTACTAT 379  
Qy 121 GluGlnTyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArgHis 140  
Db 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTCGATAGAAATTTATTAACAGAGGCAT 439  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyVal 160  
Db 440 CCTGATATGCTTACAAAATTCACATTTGGATTCCTATTTGAGAAAGTACCACCTATGTT 499  
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyLe 180  
Db 500 TTAAGGTTTCTGAAAGAAAGAACAAACAGCCAAAATGCCATATGGATTGATCTGGAATC 559  
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197  
Db 560 CATGCCAGAGAAATGGATCTCTCTGCTTCTGCTTCTGCTTCTATAGGCCATATAAATCAA 619  
Qy 197 ----- 197  
Db 620 TTCTATGGGATAATAGGGCAATATACCAATCTCTCAGGCTTCTGGAATTTCTATGTTATG 679  
Qy 198 -----AsnArgMetTrpArgLys 203  
Db 680 CCGGTGTTAATGTGACCGTTATGACTACTCATGGAAGAAAGAAATCGAATGTGAGAAAG 739  
Qy 204 AsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223  
Db 740 AACCGTTCTTTCTATCGGAACAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTGCT 799  
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyTyCysGly 243  
Db 800 TCCAAACACTGGTGTGAGGAAGGTGATCCAGTTCTCATGCTCGGAAACCTACTACTGGA 859  
Qy 244 LeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263  
Db 860 CTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGAGTGGCTAGTTCTTTGAGAAAGAAATATC 919  
Qy 264 AsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHisIleValPheProTyTy 283

Db 920 AACAGATTAAAGCATACATCAGCATGCAATTCATACATCCAGCATATAGTGTTCATAT 979  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303  
Db 980 TCCTATACAGAAAGTAAAGCAAGACCATGAGAACTGCTCTAGTAGCCAGTGAAGCA 1039  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1040 GTTCGTGCTATTGAGAAACTAGTAAATAATACCAAGGTATACATGCGCATGGCTCAGAA 1099  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343  
Db 1100 ACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAATAT 1159  
Qy 344 SerPhe-----Th 346  
Db 1160 TCGTTTCAATTAAGTAACTTCGAGATACGGGCACATACCGGATTCCTGTGCGGAGCGTTAC 1219  
Qy 346 rSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1220 ATCAACCCACCTCTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1262

RESULT 4

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerkusen, Bryan D.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed. - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores: 3.93e-214 Length: 1344  
Pred. No.: 1808.50 Matches: 355  
Score: 84.76% Conservative: 1  
Percent Similarity: 84.52% Mismatches: 4  
Best Local Similarity: 94.64% Indels: 60  
Query Match: 16 Gaps: 3  
DB:  
US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1344)  
Qy 1 MetLysLeuCyssSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 31 ATGAAGCTTTTGACGCTTCAGTCCCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 90  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 91 TTCGCGTTTCAGAGTGCCCAAGTTCAGTCTCTCTCTAGAACCTCTAGCAGGTCAA 150  
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
Db 151 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGCGAGCGGTAAACAGCTGAC 210  
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
Db 211 CTTATTGTGAAGAAAAACAAGTCCATTCTTTTGTAAATGCATCTGATGTCGACAAATGTG 270  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 271 AAAGCCCATTTAAATGTAGCCGAATTCATGACAGTGTCTTGTGAGCAGCTGGAAGAT 330  
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 331 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAAGCCCCGAGCCTCCGATCGTACTAT 390  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 391 GAAACAGTATCACTCACTAAATGAATCTTCTTGTGATAGAAATTTATTAACGTGAGGCAT 450  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 451 CCTGATATGCTTACAAAAATCCACATTCATCTCTATTGAGAGTACCCACTCTATGTT 510  
Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175  
Db 511 TTTAAGGGTTTCTTTTGAGCAGGTTTCTGCAAAAAGACAAGCAGCAAAAATGCCATATGG 570  
Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195  
Db 571 ATTGACTGTGGAATCCATGCCAGAAATCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630  
Qy 196 GlyHis----- 197  
Db 631 GGCCATATAACTCAATCTATGGGATAAAGGGCAATATACCAATCTCTCTGAGCTTGTG 690  
Qy 198 -----Asn 198  
Db 691 GATTTCATGTTATGCGCGTGTAAATGTGGATGGTTTATGACTACTCATGCAAAAAGAAAT 750

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Qy 199 ArgMetTTPArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
Db 751 CGAATGTGGAGAAAGACCGTCTTCTATCGGAACAATCATTCGATCGGACAGACTG 810
Qy 219 AsnSerIlePheValSerLysHisTTPCysGluGluGlyAlaSerSerSerCysSer 238
Db 811 AATAGGAACCTTGTCTTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCG 870
Qy 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
Db 871 GAAACCTACTGTGACTTATCTCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTTC 930
Qy 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
Db 931 TTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCCACCAT 990
Qy 279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298
Db 991 ATAGTGTTCATATTCCTATACACGAAGTAAAGCAAGAACCATGAGGAAGTGTCTCTA 1050
Qy 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
Db 1051 GTAGCCAGTGAAGCAGTTCGGCTATTGAGAAAATTAGTAAAAATACAGGTATACACAT 1110
Qy 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTyrAsp 338
Db 1111 GGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGAGGTGGGACGATTGGAICTATGAT 1170
Qy 339 LeuGlyIleLysTyrSerPhe----- 345
Db 1171 TTGGGCATCAAAATTCGTTTACAAATTTGAACTTCGAGATACGGGCACATACGGATTCTTG 1230
Qy 346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1231 CTGCCGGAGCGTTATACATCAAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1288
RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No.: US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
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; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
; US-10-115-479-67
Alignment Scores:
Pred. No.: 6,06e-214 Length: 1743
Score: 1808.50 Matches: 355
Percent Similarity: 84.76% Conservative: 1
Best Local Similarity: 84.52% Mismatches: 4
Query Match: 94.64% Indels: 60
DB: 16 Gaps: 3
US-09-980-881A-2 (1-360) x US-10-115-479-67 (1-1743)
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 20 ATGAAGCTTTGCAGCCTTCAGTCCTTGACCCATTGTTCTCTCTGTGAGCAGCATGTC 79
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 80 TTCGCGTTTCAGAGTGGCCAAGTTCAGCTGCTCTTCTTAGAACCTCTAGGCAAGTCAA 139
Qy 41 ValLeuGlnAsnLeuThrThrTyrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 140 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCGGTACAGCTGAC 199
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80
Db 200 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGCATCTCATGTGCGACAATGTG 259
Qy 81 LysAlaHisIleuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 260 AAAGCCCATTTAAATGTGACGGAATTCATGCAAGTGTCTTGTGTCAGACGTGGAAGAT 319
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 320 CTTATTCAACAGCAGATTTCACACGACACAGTCAGACCCCGAGCCTCCGCATCTACTAT 379
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHis 140
Db 380 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATATACTAGAGGCAT 439
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 440 CCTGATATGCTTACAAAAATCCACATTTGGATTCCTCATTTTGAGAAAGTACCCACTTATGTT 499
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Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaLeuTip 175
Db 500 TTAAGGGTTCTTTGAGCAGGTTCTTGAAAAGAACAGCAGCAAAATGCGCATGG 559
Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
Db 560 ATTGACTGTGGAATCCATGCCAGAGATGGATCTCTCTGCTTTCTGCTGTGGTTTCA 619
Qy 196 GlyHis----- 197
Db 620 GGCCATATACTCAATTCATGGGATAATAGGCAATATACCAATCTCTGAGGCTTTGTG 679
Qy 198 -----Asn 198
Db 680 GATTTCATGTTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAGAAAT 739
Qy 199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
Db 740 CGAATGTGGAGAAAGACCGTTCTTTCTATGCGAACAATCATTCGATCGGACAGACCTG 799
Qy 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238
Db 800 AATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAGGTGCATCCAGTTCTCATGCTCG 859
Qy 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
Db 860 GAAACCTACTGTGACCTTATCTCTGAGTCAGAACAGAGTGAAGGAGGTGGCTAGTTTC 919
Qy 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
Db 920 TTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCAT 979
Qy 279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298
Db 980 ATAGTGTTCATATTCCTATACAGAACTTAAAGCAAGTAAAGCAAGCACTGTCTCTA 1039
Qy 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
Db 1040 GTACCCAGTGAGCAGTTCGTGCTTATGAGAAATTTAGTAAATATACAGGTATACAT 1099
Qy 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
Db 1100 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGACGATTGGATCTATGAT 1159
Qy 339 LeuGlyIleLysTyrSerPhe----- 345
Db 1160 TTGGGCATCAATATTCGTTTACAATTCGAATTCGAGATACGGGCACATACGGATTCTTG 1219
Qy 346 -----ThrSerAnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1220 CTGCGGAGCGGTTACATCAACCCACTGTAGAGAGCTTTTGCGGTGCTCTTAAAA 1277

RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 2003-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (1)..(1269)
US-10-379-836-1
Alignment Scores:
Pred. No.: 2,79e-204 Length: 1272
Score: 1729.00 Matches: 338
Percent Similarity: 83.37% Conservative: 8
Best Local Similarity: 81.45% Mismatches: 14
Query Match: 90.48% Indels: 55
DB: 15 Gaps: 2

US-09-980-881A-2 (1-360) x US-10-379-836-1 (1-1272)
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 1 ATGAAGCTTTGCACTCTTGAGTCCCTTGACGTCCTTGACCATTTGCTCTCTGTGAGCAGCATGTC 60
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 61 TTCGCGTTTCAGAGTGGCCAGGTTCTAG: TGCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
Qy 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 121 GTGCTACAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCGGAC 180
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80
Db 181 CTTATTGAGAGAAACAAACAGTCCAAATTTTGTAAATTCATCTGATGTCGCAATGTG 240
Qy 81 LysAlaHisLeuAsnValSerGlyIleP: cCysSerValLeuLeuAlaAspValGluAsp 100
Db 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAAGTCTCTGTCGACAGATGTGGAAGAT 300
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 301 CTTATTCAACAGCAGATTTTCCACAGCACAGTCAAGCCCCCGAGCCCTCCGATCGTACTAT 360
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 361 GAACGATATCACTCACTAAATGAAATCTMTTCTTGGATGAACTTATACTAGAGAGAT 420
Qy 141 ProAspMetLeuThrLysIleHisIleG: ySerSerPheGluLysTyrProLeuTyrVal 160
Db 421 CCTGATATGCTTACAAAATCCACATTCATCTCTCTATGAGAGAACCCACCTTTATGTT 480
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 481 TTAAGGTTTCTGGAAGAAACAAACAG: CAAAAATGCCATGTGGATTGACTGTGGAATC 540
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db 541 CATGCCAGAGAAATGGATCTCCCTGCTT: CTGCTTGTGGTTTCATAGGCCATATAACTGAA 600
Qy 197 ----- 197
Db 601 TACTACGGGTAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTCTATGTTATG 660
Qy 198 -----AsnArgMetTrpArgLys 203
Db 661 CCAGTGGTTAAATGTGGATGGTTATGACTTACTCATGGAAGAAAGAAATGTCGAGAAAG 720
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 721 AACCGTTTCTTATGCGAACAATCGTTTCAUCGGAACAGACCTGAACAGGAACTTTGCG 780
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly 243
Db 781 TCCAAACACCTGGTGTGAGGAAGGTGCAT: CAGTTTCTCTGCTCGGAAACCTACTGTGGA 840
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
Db 841 CTTTATCTCTGAGTCAGAACAGAAAGCGA: GGCGGTGGCTAAATTTCTTGAAGAAATATC 900
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Db 571 ----- 571
Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
Db 572 ---TGTGGATTTATCTCGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGA 628
Qy 261 ArgSerIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
Db 629 AGAAATATCAACCAAGATTAAAGCATACATCAGCATGCATTCATCACTCCAGCATATAGT 688
Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
Db 689 TTTCATATTCCTATACACGAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTAGCC 748
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
Db 749 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACCAGGTATACACATGGCCAT 808
Qy 321 GlySerGlnThrLeuTyrLeuAlaProGlyGlyGlyAspAspThrIleTyrAspLeuGly 340
Db 809 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATGGATCTATGATTGGGC 868
Qy 341 IleLysTyrSerPhe----- 345
Db 869 ATCAAAATATTCGTTTACAAATTGAACCTTCGAGATACGGGCACATACGGATTCTTGCTGCCG 928
Qy 346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 929 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGGTGTCTCTAAAA 980

RESULT 8
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, 'Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
```

```
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.: 1,27e-162 Length: 1132
Score: 1393.50 Matches: 283
Percent Similarity: 67.38% Conservative: 0
Best Local Similarity: 67.38% Mismatches: 3
Query Match: 72.92% Indels: 134
DB: 16 Gaps: 4
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US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1132)

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Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 41 ATGAGCTTTGCAGCCTTGCGAGTCTTGACCCATTGTTCTCTCTGTGAGCAGCATGTC 100
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTGCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTTAGCGAAGTTCAA 160
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACGCTGAC 220
Qy 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80
Db 221 CTTATTGTGAAGAAAAACAAAGTCCATTTTTGTGTAATGCATCTGTATGTCGACATGTG 280
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGTGGCAGACGTTGGAAGAT 340
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 341 CTTATTCAACAGCAGATTTCACACGACACAGTACGCCCGCCGCTCCGCGATGCTACTAT 400
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTATATACTGAGAGGCAT 460
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 461 CCTGATATGCTTACAAAAATCCACATGTCATCTCATTTTGAAGATACCCCACTCTATGTT 520
Qy 161 LeuLys-----ValSerGlyLysGlnThrAlaLysAsnAlaIleTyr 175
Db 521 TTAAGGGTTCTTTGAGCAGGTTTCTGAAAAAGAACAGCAGCAAAATATGCCATATGG 580
Qy 176 IleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIle 195
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; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1141
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1141

Alignment Scores:
Pred. No.: 1,86e-66 Length: 1332
Score: 621.50 Matches: 134
Percent Similarity: 53.66% Conservative: 71
Best Local Similarity: 35.08% Mismatches: 132
Query Match: 32.52% Indels: 45
DB: 9 Gaps: 8

US-09-980-881A-2 (1-360) x US-09-954-456-1141 (1-1332)
Qy 3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
Db 24 ATGTGGCACTCTTGGTCTTGGTACTGTGGCCCTGGCATCTCTCTCATCATGGTGGTGGAG 83
Qy 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
Db 84 CACTTTGAAGCGGAGAAGGTGTTCCGTGTTAAAGTGAAGATGAAATACATTAACATA 143
Qy 42 LeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeu 61
Db 144 ATCCGGAGTGGCCAGCAGCAGCCAGATTTGACTTCTGGAAGCCAGATTTCTGTACACAA 203
Qy 62 IleValIleValIleValHisPheValAsnAlaSerAspValAspValLys 81
Db 204 ATCAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAGATGACTGTCTACTGTGGAG 263
Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
Db 264 AATGTTCTAAAGCAGATGAATCACTACATACAGTACTGTAAGCAACCTGAGAAATGTG 323
Qy 102 IleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
Db 324 GTGGAGGCTCAGTTTGATAGCCGGT-----CGTGCACAGGACACAGTATATGAG 374
Qy 122 GlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisPro 141
Db 375 AAGTACACAAAGTGGGAAACGATAGAGGCTTGACTCAACAGTCCGCCACTGAGAAATCCA 434
Qy 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
Db 435 GCCTCATCTTCGCAAGTGTATTCGGAACACACATTTGAGGAGCGCGCTATTACTCTCTG 494
Qy 162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIleHis 181
Db 495 AAGGTT---GGCAAGCTGGACAAAATAAGCTGCCATTTTCATGAGCTGTGGTTCAT 551
Qy 182 AlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 195
Db 552 GCACAGAGTGGATTTCTCTCCATCTCCAGTGGTGTGTTGTAAGAGAGGCTGTTCGTACC 611
Qy 195 ----- 195
Db 612 TATGGAGTGGATCCAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCCT 671
Qy 196 -----GlyHis-----AsnArgMetTyrArgLysAsn 204
Db 672 GTGCTCAATATTGATGGCTACATCTACCTCGACCAAGAGCGGATTTTGGAGAAAGACT 731
Qy 205 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224
Db 732 CGCTCCACCCACTACTGGATCT---AGCATTTGGCAGACAGCCCAACAGAAATTTT---GAT 785
Qy 225 LysHisTyrCysGluGluAlaSerSerSerCysSerGluThrTyrCysGlyLeu 244
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RESULT 12

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US-09-954-456-1141
; Sequence 1141, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
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Db 786 GCTGTTGGTGTGAAATTGAGCGCTCTCGAAACCCCTGTGTGATGAAACTTACTGTGGACCT 845  
 Qy 245 TyrProGlnSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264  
 Db 846 GCCGACAGTCTGAAAGAGGACCAAGCCCTGGCTGATTTCATCCGCAACAACTCTCT 905  
 Qy 265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284  
 Db 906 TCATATCAAGGCAATCTGCAATCCACTCGTACTCCCAATGATGATCTACCTTACTCA 965  
 Qy 285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304  
 Db 966 TATGCTTACAACTCGGTGAGAACAACTGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTG 1025  
 Qy 305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324  
 Db 1026 AAGAACTT---GCCCTACTGCACGGCACCACCAAGTACACATATGGCCCGGGAGCTACAACA 1082  
 Qy 325 LeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSer 344  
 Db 1083 ATCTATCTGCTGCTGGGGCTCTGACGACTTGGCTTATGACCAAGGAATCAGATATTC 1142  
 Qy 345 PheThr 346  
 Db 1143 TTCACC 1148  
 RESULT 13  
 US-10-341-434-187  
 ; Sequence 187, Application US/10341434  
 ; Publication No. US20030215835A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes  
 ; FILE REFERENCE: 9U 204 205 R1  
 ; CURRENT APPLICATION NUMBER: US/10/341.434  
 ; CURRENT FILING DATE: 2003-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/348,164  
 ; PRIOR FILING DATE: 2002-01-15  
 ; PRIOR APPLICATION NUMBER: US 60/348,119  
 ; PRIOR FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 238  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 187  
 ; LENGTH: 1633  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (12)..(1262)  
 ; OTHER INFORMATION:  
 ; US-10-341-434-187  
 Alignment Scores:  
 Pred. No.: 3,48e-66 Length: 1633  
 Score: 620.50 Matches: 130  
 Percent Similarity: 54.19% Conservative: 77  
 Best Local Similarity: 34.03% Mismatches: 128  
 Query Match: 32.47% Indels: 47  
 DB: 15 Gaps: 8  
 US-09-980-881A-2 (1-360) x US-10-341-434-187 (1-1633)  
 Qy 5 SerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla----- 22  
 Db 9 ACCATGAGGCTCATCTCGCTGTGGTGTGCTTACCCTCTTGTCAATTTGCTCTGTGC 68  
 Qy 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41  
 Db 69 CGCTTTGACGGGAGAGAGTGTTCGGGTGAGCCCGCAGGATGAAACAAACGACGACATC 128  
 Qy 42 LeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeu 61  
 Db 129 ATAAAGGACTTGGCCAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACCAC 188

Qy 62 IleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81  
 Db 189 GTAGCTGCTAATATGATGTGTGATTTCCAGATTAGTGAAGAATCCCAAGCATCCAG 248  
 Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101  
 Db 249 TCTGCTTGGATCAAAATAAATGCACTATGAATCTTGATTCATGATCTTACAAGAAGAG 308  
 Qy 102 IleGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
 Db 309 ATTGAGAAACAGTTGATGTTAAAGAAGATATCCAGCGCAGGCACAGC-----TAC 359  
 Qy 121 GluGluTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHis 140  
 Db 360 GCAAAATACAAATTAATTTGGGAAAGATTTGGCTTGGACTGAAAGAATGATGATATAT 419  
 Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
 Db 420 CCTGAATGGTCTCTCGTATTAAATTTGATCTACTGTTGAAGATAATCCACTATATGTT 479  
 Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleThrPleAspCysGlyIle 180  
 Db 480 CTGAGATT---GGGGAAGAAAGATGAAGAAAGAGCTATTTTATGGATTGTGCATT 536  
 Qy 181 HisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 195  
 Db 537 CACGACAGAGATGGGTCTCCCGAGCATTTCTGCAGTGGTTGTCTATCAGGCAACCAA 596  
 Qy 195 ----- 195  
 Db 597 ACTTATGGGAGAAACAAATTAATGACCAAACTCTTGACCGAATGAATTTTATCTTCT 656  
 Qy 196 -----GlyHis-----AsnArgMetTyrArgLys 203  
 Db 657 CTTGTGTTCAATGTTGATGGATATATTGTCATGGACAAAGAACCGCATGTGGAGAAA 716  
 Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223  
 Db 717 AATCGTTTCAAGAACCAAACTCCAATCATCGGCACTGACCTCAACAGGAATTT--- 773  
 Qy 224 SerLysHisTyrCysGluGluGlyAlaSerSerCysSerSerGluThrTyrCysGly 243  
 Db 774 AATGCTTCATGGAACCTCCATTCCTAAACACCAATGACCCATGTGCAGATACTATCGGGC 833  
 Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263  
 Db 834 TCTGCACACAGTCCGAGAAAGAGAGAGAGTGTCTCAATAATTTTATAGAACCCACTG 893  
 Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
 Db 894 AATGAAATCAAGGTTTACATCATCTCCATTCCTTACTCCAGATGATTTGTTTCCCTAT 953  
 Qy 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303  
 Db 954 GGATATACATCAAACTGCCACCTAACCATGAGACTTGGCCAAAGTTGCAAGATTGGC 1013  
 Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
 Db 1014 ACTGATGTTCTA---TCAACTCGATATGFAACCCGCTACATCTATGCGCCCAATAGAATCA 1070  
 Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyr 343  
 Db 1071 ACAATTTACCGATATCAGGTTCTTCTTAGACTGGGCTTATGACCTGGGCAATCAACAC 1130  
 Qy 344 SerPhe 345  
 Db 1131 ACATTT 1136  
 RESULT 14  
 US-10-116-802-95  
 ; Sequence 95, Application US/10116802  
 ; Publication No. US20030065157A1

GENERAL INFORMATION:  
APPLICANT: Amy Lasek  
TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER  
FILE REFERENCE: PA-0045 US

CURRENT APPLICATION NUMBER: US/10/116,802

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 60/281,593

PRIOR FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 519

SOFTWARE: PERL Program

SEQ ID NO 95

LENGTH: 1740

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No: 1656674CBI

US-10-116-802-95

Alignment Scores:

Pred. No.:	3,87e-66	Length:	1740
Score:	620.50	Matches:	130
Percent Similarity:	54.19%	Conservative:	77
Best Local Similarity:	34.03%	Mismatches:	128
Query Match:	32.47%	Indels:	47
DB:	14	Gaps:	8

US-09-980-881A-2 (1-360) x US-10-116-802-95 (1-1740)

Qy	5	SeuLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla-----	22
Db	3	ACCATGAGGCTCTCCCTGCGCTGCTGGTTCCTACCACTCTTGCAATTGCTCCTGTC	62
Qy	23	---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal	41
Db	63	CGCTTTGACAGGAGAGAGTGTTCGCGTGAGGCCCGAGGATGAAACCAAGCAGCATC	122
Qy	42	LeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAspLeu	61
Db	123	ATAAGAGACTTGGCCAAACCAATGACTTGCATCTTCTGGTATCCAGTGCCACCCACCAC	182
Qy	62	IleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLys	81
Db	183	GTAGCTCTAATATGATGGTGGATTTCGAGTGTAGTGAGAAGGAATCCCAAGCATCCAG	242
Qy	82	AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu	101
Db	243	TCTGCTTGGATCAAAATAAAATGCATATGAAATCTTGATTCATGATCTTACAAGAAGAG	302
Qy	102	IleGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrr	120
Db	303	ATTGAGAAACAGTTTGATTTAAAGAAGATATCCAGGAGGACAGC-----TAC	353
Qy	121	GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheThrGluArgHis	140
Db	354	GCAAAATACAAATATTCGGAAGAAAGATGTGCTGGACTGAAAGATGATGATAAGTAT	413
Qy	141	ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrVal	160
Db	414	CCTGAATGGTCTCTCGTATTAATAATGGATCTACTCTTGAAGATATATCCACTATGTT	473
Qy	161	LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle	180
Db	474	CTGAAGATT---GGGGAAGAAAGATGAAAGAAAGAGGCTATTTTATGGATTGGGCATT	530
Qy	181	HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle-----	195
Db	531	CACGACAGAAATGGGTCTCCCGAGCATCTCGCAGTGGTGTCTCATCAGGACCAAAA	590
Qy	195	-----	195
Db	591	ACTTATGGGAGAAACAAAATTTATGACCAAACTCTTGGACCAATGAAATTTTATCATCTCT	650

Qy	196	-----GlyHis-----AsnArgMetTrpArgLys	203
Db	651	CCTGTGTTCAATGTTGATGATATATTTGGTCATGACAAAGAACCGCATGTGAGAAAA	710
Qy	204	AsnArgSerPheTyrrAlaAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal	223
Db	711	AATCGTTTCCAAGAACCAAACTCCAATGCATCGGCACCTGACCTCAACAGGAATTTT---	767
Qy	224	SerLysHisTrpCysGluGlyAlaSerSerCysSerSerSerGluThrTyrrCysGly	243
Db	768	AATGCTTCATGGAACTCCATTTCTAACCAACCAATGACCCATGTGCAGATACTATCGGGC	827
Qy	244	LeuTyrrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle	263
Db	828	TCTGCACAGAGTCCGAGAAAGAGAGAAAGCTGTCACTAATTTTATTAGAACCCACTG	887
Qy	264	AsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPheProTyrr	283
Db	888	AATGAAATCAAGGTTTACATCACCTTCCATTTCTTACTCCAGATGCTATTGTTTCCCTAT	947
Qy	284	SerTyrrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla	303
Db	948	GGATATACATCAAACTGCCACCTAACCATGAGACTTGGCCAAAGTTGCAAGATGGC	1007
Qy	304	ValArgAlaIleAspLysThrSerLysAsnThrArgTyrrThrHisGlyHisGlySerGlu	323
Db	1008	ACTGATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGCCCCAATAGAATCA	1064
Qy	324	ThrLeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrrAspLeuGlyIleLysTyrr	343
Db	1065	ACAATTTACCGCATATCAGGTTCTCTTTAGACTGGGCTTATGACCTGGGCATCAACAC	1124
Qy	344	SerPhe	345
Db	1125	ACATTT	1130

## RESULT 15

US-10-229-546-3

Sequence 3, Application US/10229546

Publication No. US20030082649A1

GENERAL INFORMATION:

APPLICANT: Weich, Nadine S.

APPLICANT: Carroll, Joseph M.

APPLICANT: Millennium Pharmaceuticals, Inc.

TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR

FILE REFERENCE: MP101-156P1RNM

CURRENT APPLICATION NUMBER: US/10/229,546

CURRENT FILING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: 60/316,575

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1254

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1254)

US-10-229-546-3

Alignment Scores:

Pred. No.:	2,99e-66	Length:	1254
Score:	619.50	Matches:	130
Percent Similarity:	54.07%	Conservative:	76
Best Local Similarity:	34.12%	Mismatches:	128
Query Match:	32.42%	Indels:	47
DB:	14	Gaps:	8

US-09-980-881A-2 (1-360) x US-10-229-546-3 (1-1254)

Qy 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla----- 22

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Db      1  ATGAGGCTCATCTGCTGCTGGGTTTGATTGCTACCACTTTGCAATTGCTCTGTCCGC 60
Qy      23  PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 42
Db      61  TTTGACAGGAGAGAGGTGTTCCGCGTGAAGCCCGAGGATAAAACAAGCAGACATCAT 120
Qy      43  GlnAsnLeuThrThrThrThrGluLeuValLeuTrpGlnProValThrAlaAspLeu 62
Db      121  AAGGACTTGCCCAAAACCAATGAGCTTGACTTCTGGTATCCAGGTGCCACCCACACGTA 180
Qy      63  ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 82
Db      181  CTTGCTTAATATGATGGTGGATTTCGAGTTAGTGAGAGGAATCCCAAGCCATCCAGTCT 240
Qy      83  HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 102
Db      241  GCCTTGGATCAAAATAAATGCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300
Qy      103  GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
Db      301  GAGAAACAGTTTGATGTTAAGAAGATATCCAGGCGAGGCACAGC-----TAGCA 351
Qy      122  GlnTyrHisSerLeuAsnGluLeuTyrSerTyrIleGluPheIleThrGluArgHisPro 141
Db      352  AAATACATAATTTGGGAAAGATTTGGCTTGGACTGAAAGATGATGGATAAGTATCCT 411
Qy      142  AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
Db      412  GAAATGGTCTCTCGTATTAAATTTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471
Qy      162  LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181
Db      472  AAGATT---GGGAAAGAGATGAAGAAGAAAGAGCTATTTTATGGATTGTGGCATTCAC 528
Qy      182  AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db      529  GCACGAGATGGGTCTCCCGAGCATCTGCGAGTGGTTGTCTATCAGGCAACCAAAACT 588
Qy      195  ----- 195
Db      589  TATGGGAGAAACAAATTATGACCAAACTCTGGACCGAATGAATTTTACATTCTTCCT 648
Qy      196  -----GlyHis-----AsnArgMetTrpArgLysAsn 204
Db      649  GTGTTCAATGTTGATGATATATTTGGTCATGGACAAGAACCGCATGTGGAGAAAAAT 708
Qy      205  ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer 224
Db      709  CGTTCCAAGAACCAAAACTCCAATGCATCGCACTGACCTCAACAGGAATTTT---AAT 765
Qy      225  LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 244
Db      766  GCTTCATGGAACCTCAATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825
Qy      245  TyrProGlnSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 264
Db      826  GCACCAAGAGTCCGAGAAAGAGACGAAGAGCTGCTCAATTTTATTAGAACCCCTGAAT 885
Qy      265  GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284
Db      886  GAAATCAAGGTTTACATCCTCCATCCCTACTCCAGATGCTATTTGTTTCCCTATGGA 945
Qy      285  TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
Db      946  TATACATCAAAACTGCCACCACTTAACCATGAGGACTTGGCCAAAGTTGCAAGATTGGCACT 1005
Qy      305  ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324
Db      1006  GATGTTCTA---TCAACTCGATATGAACCCGCTACATCTATGGCCCAATAGAAATCAACA 1062
Qy      325  LeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344
```

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Db      1063  ATTTACCCGATATCAGGTTCTTCTTTAGATGGGCTTATGACCTGGGCATCAAAACACACA 1122
Qy      345  Phe 345
Db      1123  TTT 1125
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Search completed: October 31, 2004, 08:40:28  
Job time : 640.949 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:34:50 ; Search time 25.7797 Seconds  
(without alignments)  
869.503 Million cell updates/sec

Title: US-09-980-881A-3

Perfect score: 1798

Sequence: 1 FOSGQVLAALPRTSRQVQL.....IKYSFTSNPPVEXKLLPLSLK 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1717	95.5	386	4	US-09-813-133A-2
2	1699.5	94.5	423	1	US-07-649-591B-3
3	1699.5	94.5	423	1	US-08-277-540-3
4	1699.5	94.5	423	1	US-08-430-787A-3
5	1699.5	94.5	423	2	US-08-869-057-2
6	1688.5	93.9	423	4	US-09-813-133A-4
7	646.5	36.0	404	1	US-08-696-139-2
8	637.5	35.5	415	2	US-08-860-882A-57
9	637.5	35.5	415	4	US-09-011-769A-39
10	637.5	35.5	424	4	US-09-011-769A-56
11	632	35.2	417	1	US-07-649-591B-7
12	632	35.2	417	1	US-08-277-540-7
13	632	35.2	417	1	US-08-430-787A-7
14	622	34.6	417	1	US-07-649-591B-6
15	622	34.6	417	1	US-08-277-540-6
16	622	34.6	417	1	US-08-430-787A-6
17	622	34.6	417	4	US-09-917-254-66
18	619.5	34.5	716	3	US-09-171-945-125
19	612	34.0	437	4	US-09-675-305-10
20	612	34.0	437	4	US-10-200-344-10
21	610	33.9	307	2	US-08-782-760-6
22	610	33.9	307	5	PCT-US96-00995-6
23	609.5	33.9	396	1	US-07-649-591B-4
24	609.5	33.9	396	1	US-08-277-540-4
25	609.5	33.9	396	1	US-08-430-787A-4
26	582	32.4	306	1	US-08-696-139-4
27	567	31.5	329	4	US-09-011-769A-51

28	567	31.5	349	4	US-09-011-769A-47	Sequence 47, Appl
29	560	31.1	349	4	US-09-011-769A-60	Sequence 60, Appl
30	559	31.1	349	4	US-09-011-769A-64	Sequence 64, Appl
31	554	30.8	399	4	US-09-710-099-8	Sequence 8, Appl
32	554	30.8	399	4	US-10-200-910-8	Sequence 8, Appl
33	549.5	30.6	417	1	US-07-649-591B-8	Sequence 8, Appl
34	549.5	30.6	417	1	US-08-277-540-8	Sequence 8, Appl
35	549.5	30.6	417	1	US-08-430-787A-8	Sequence 8, Appl
36	549	30.5	613	3	US-09-171-945-113	Sequence 113, App
37	534.5	29.7	350	4	US-09-675-305-12	Sequence 12, Appl
38	534.5	29.7	350	4	US-10-200-344-12	Sequence 12, Appl
39	532.5	29.6	419	1	US-07-649-591B-5	Sequence 5, Appl
40	532.5	29.6	419	1	US-08-277-540-5	Sequence 5, Appl
41	532.5	29.6	419	1	US-08-430-787A-5	Sequence 5, Appl
42	527.5	29.3	436	4	US-09-710-099-6	Sequence 6, Appl
43	527.5	29.3	436	4	US-10-200-910-6	Sequence 6, Appl
44	516.5	28.7	417	3	US-08-640-906-4	Sequence 4, Appl
45	516.5	28.7	417	3	US-09-395-936-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-813-133A-2

; Sequence 2, Application US/09813133A

; Patent No. 6455294

; GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: CLO01173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Human

; US-09-813-133A-2

Query Match 95.5%; Score 1717; DB 4; Length 386;  
Best Local Similarity 99.4%; Pred. No. 8.3e-181;  
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	FOSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTADLVKKQVHFFVNASDVNVKA	60
DB	23	FOSGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTADLVKKQVHFFVNASDVNVKA	82
QY	61	HLNVSIGPCSVLLADVDELIIQQISNDTVSPRASAYYEQYHSLNIYISWIEFITERHPD	120
DB	83	HLNVSIGPCSVLLADVDELIIQQISNDTVSPRASAYYEQYHSLNIYISWIEFITERHPD	142
QY	121	MLTKIHIGSSFEKPYLVKVSKEQTAKNAWIDCGIHAREWISPAFCLWFIHNRMR	180
DB	143	MLTKIHIGSSFEKPYLVKVSKEQTAKNAWIDCGIHAREWISPAFCLWFIHNRMR	202
QY	181	KNRSFYANNHCITGLNRFNFASKHWCCEGASSSSCSETCYGLYPESEPEVKAVASFLRN	240
DB	203	KNRSFYANNHCITGLNRFNFASKHWCCEGASSSSCSETCYGLYPESEPEVKAVASFLRN	262
QY	241	INQIKAYISMHSYQSHIVFPYSTRSKSDHELSLVASEAVRAIEKTSKNTRYTHGHGS	300
DB	263	INQIKAYISMHSYQSHIVFPYSTRSKSDHELSLVASEAVRAIEKTSKNTRYTHGHGS	322
QY	301	ETLYLAPGGDDMIYDLGIKYSFT	324
DB	323	ETLYLAPGGDDMIYDLGIKYSFT	346

RESULT 2

US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/466-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; US-07-649-591B-3

Query Match 94.5%; Score 1699.5; DB 1; Length 423;  
Best Local Similarity 89.8%; Pred. No. 8.2e-179;  
Matches 324; Conservative 0; Mismatches 0; Indels 37; Gaps 1;  
  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEI VLWQPVTDADLVKKKQVHFFVNASDVNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEI VLWQPVTDADLVKKKQVHFFVNASDVNDVKA 82  
  
Qy 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
  
Qy 121 MLTKIHIGSSPEKPYLVLVKVSKEQTAKNAIWDGCIHAREWISPAFCIWFIGH----- 175  
Db 143 MLTKIHIGSSPEKPYLVLVKVSKEQTAKNAIWDGCIHAREWISPAFCIWFIGHITQFY 202  
  
Qy 176 -----NRMWRKRSFYANNHCIGTDLNRNFSK 203  
Db 203 GIIGQVTLNLLRLVDFYVMPVNVVDGYDYSWKKNRMWRKRSFYANNHCIGTDLNRNFSK 262  
  
Qy 204 HWCEEGASSSSCSSTCYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPYSY 263  
Db 263 HWCEEGASSSSCSSTCYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPYSY 322  
  
Qy 264 TRSKSKDHEELSLVASAVRAIEKTSKNRTHGHGSETLYLAPGGDDMIYDLGIKYSF 323  
Db 323 TRSKSKDHEELSLVASAVRAIEKTSKNRTHGHGSETLYLAPGGDDMIYDLGIKYSF 382  
  
Qy 324 T 324  
Db 383 T 383

RESULT 3  
US-08-277-540-3  
; Sequence 3, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-277-540-3

Query Match 94.5%; Score 1659.5; DB 1; Length 423;  
Best Local Similarity 89.8%; Pred. No. 8.2e-179;  
Matches 324; Conservative 0; Mismatches 0; Indels 37; Gaps 1;  
  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEI VLWQPVTDADLVKKKQVHFFVNASDVNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEI VLWQPVTDADLVKKKQVHFFVNASDVNDVKA 82  
  
Qy 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
  
Qy 121 MLTKIHIGSSPEKPYLVLVKVSKEQTAKNAIWDGCIHAREWISPAFCIWFIGH----- 175  
Db 143 MLTKIHIGSSPEKPYLVLVKVSKEQTAKNAIWDGCIHAREWISPAFCIWFIGHITQFY 202  
  
Qy 176 -----NRMWRKRSFYANNHCIGTDLNRNFSK 203  
Db 203 GIIGQVTLNLLRLVDFYVMPVNVVDGYDYSWKKNRMWRKRSFYANNHCIGTDLNRNFSK 262  
  
Qy 204 HWCEEGASSSSCSSTCYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPYSY 263  
Db 263 HWCEEGASSSSCSSTCYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPYSY 322

Qy 264 TRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGKYSF 323  
|  
Db 323 TRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGKYSF 382  
|  
Qy 324 T 324  
|  
Db 383 T 383  
|  
RESULT 4  
US-08-430-787A-3  
; Sequence 3, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 01-FEB-91  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 14-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasek, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-430-787A-3  
Query Match 94.5%; Score 1699.5; DB 1; Length 423;  
Best Local Similarity 89.8%; Pred. No. 8.2e-179;  
Matches 324; Conservative 0; Mismatches 0; Indels 37; Gaps 1;  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTADLVKKKQVHFFVNASDVNVKA 60  
|  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTADLVKKKQVHFFVNASDVNVKA 82  
|  
Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYEQYHSNLEYISWIEFITERHPD 120  
|  
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYEQYHSNLEYISWIEFITERHPD 142  
|  
Qy 121 MLTKIHGSSFEKYPVLVVKVSGKEQAKNAIWDGCIHAREWISPAFCLWFIGH---- 175  
|

Db 143 MLTKIHGSSFEKYPVLVVKVSGKEQAKNAIWDGCIHAREWISPAFCLWFIGHITQFY 202  
|  
Qy 176 -----NRMWRKNRSFYANNHCIGTDLNRNPASK 203  
|  
Db 203 GIIGQYTNLLRLVDFVMPVNVVDGYDSWKQNRMRKNRSFYANNHCIGTDLNRNPASK 262  
|  
Qy 204 HMCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSY 263  
|  
Db 263 HMCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIYFPYSY 322  
|  
Qy 264 TRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGKYSF 323  
|  
Db 323 TRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGKYSF 382  
|  
Qy 324 T 324  
|  
Db 383 T 383  
|  
RESULT 5  
US-08-869-057-2  
; Sequence 2, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Plasma  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 23..401  
; US-08-869-057-2  
Query Match 94.5%; Score 1699.5; DB 2; Length 423;  
Best Local Similarity 89.8%; Pred. No. 8.2e-179;  
Matches 324; Conservative 0; Mismatches 0; Indels 37; Gaps 1;  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTADLVKKKQVHFFVNASDVNVKA 60  
|  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTADLVKKKQVHFFVNASDVNVKA 82  
|

Qy 61 HLNVSIGIPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
Qy 121 MLTKIHIGSSPEKYPVLVVKVSGKEQAKNAIWDGCHAREWISPAFCLWFIGH---- 175  
Db 143 MLTKIHIGSSPEKYPVLVVKVSGKEQAKNAIWDGCHAREWISPAFCLWFIGHITQFY 202  
Qy 176 -----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
Db 203 GIIGQYTNLLRLVDFYVMPVNVVDGYDSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262  
Qy 204 HWCHEGASSSCSTYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 263  
Db 263 HWCHEGASSSCSTYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 322  
Qy 264 TRSKSKDHEELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDMYDILGIKYSF 323  
Db 323 TRSKSKDHEELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDMYDILGIKYSF 382  
Qy 324 T 324  
Db 383 T 383  
RESULT 6  
US-09-813-133A-4  
; Sequence 4, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-4  
Query Match 93.9%; Score 1688.5; DB 4; Length 423;  
Best Local Similarity 89.2%; Pred. No. 1.4e-177;  
Matches 322; Conservative 0; Mismatches 2; Indels 37; Gaps 1;  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIWLQPVPTADLIIVKKQVHFFVFNASDVNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIWLQPVPTADLIIVKKQVHFFVFNASDVNDVKA 82  
Qy 61 HLNVSIGIPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
Qy 121 MLTKIHIGSSPEKYPVLVVKVSGKEQAKNAIWDGCHAREWISPAFCLWFIGH---- 175  
Db 143 MLTKIHIGSSPEKYPVLVVKVSGKEQAKNAIWDGCHAREWISPAFCLWFIGHITQFY 202  
Qy 176 -----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
Db 203 GIIGQYTNLLRLVDFYVMPVNVVDGYDSWKKNRMWRKNRSFYANNHCIGTDLNRNFASK 262  
Qy 204 HWCHEGASSSCSTYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 263  
Db 263 HWCHEGASSSCSTYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 322  
Qy 264 TRSKSKDHEELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDMYDILGIKYSF 323  
Db 323 TRSKSKDHEELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDMYDILGIKYSF 382

Qy 324 T 324  
Db 383 T 383  
RESULT 7  
US-08-696-139-2  
; Sequence 2, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hershberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: US 08/153,258  
; APPLICATION NUMBER: 16-NOV-1993  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 404 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-696-139-2  
Query Match 36.0%; Score 646.5; DB 1; Length 404;  
Best Local Similarity 38.0%; Pred. No. 1.8e-62;  
Matches 137; Conservative 60; Mismatches 121; Indels 43; Gaps 6;  
Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIWLQPVPTADLIIVKKQVHFFVFNASDVNDVKA 60  
Db 10 FEQEKVFRNVVEDNDISLHLELASTQIDFWKPDSTVQIKPHSTVDVFRVKAEDILAVE 69  
Qy 61 HLNVSIGIPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 70 FLEQNELOVEVLNLLRSVLEAQFDSRV---RTTGHSEYKYNWETIEAWTKQVTSNP 126  
Qy 121 MLTKIHIGSSPEKYPVLVVKVSGKEQAKNAIWDGCHAREWISPAFCLWFIGH---- 173  
Db 127 LISRTAIGTTFGLNNIYLLKV-GKPGFNKPAIFMDCGFHAREWISHAFCQWVREAVLTY 185  
Qy 174 -----GH-----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
Db 186 GYBSHMTFELKLDFFVLPVINDIGYIYTWKRMWRKTESTNAGTTCIGTDPNRF-DA 244







```
;
;
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
US-07-649-591B-7

Query Match 35.2%; Score 632; DB 1; Length 417;
Best Local Similarity 38.2%; Pred. No. 7.4e-61;
Matches 138; Conservative 57; Mismatches 122; Indels 44; Gaps 7;

QY 1 FQSGQVLAALPRTSROVQVQLNLTITTYEIVLWQPVTDALIVKKQVHFFVNASDNDVKA 60
DB 21 FDREKVFVKLQNEKHASVLKNTLSIELDFWYDPAIDHDAVNMVDFRVSEKESQTIQS 80
QY 61 HLNVSIGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYEYQVHSLNEIYSWIEFITERHP 119
DB 81 TLEQHKIHYEILIHDLQEEIEKQDFVKDEIAGRHS---YAKYNDWDKIVSWTEKMLEKHP 137
QY 120 DMLTKIHIGSSFYKLYVVLKVSKEQTAKNAIWDGCIHAREWISPAFCLEWFI----- 173
DB 138 EMVSRIKIGSTVEDNPLYVLKI-GKKGGERKAIFMDCGIHAREWISPAFCQWFVYQATKS 196
QY 174 -GHN-----RMWRKNRSFYANNHCIGTDLNRNFS 202
DB 197 YGKNKIMTKLDRMNFVLPVFNVDGYIWSWTQDRMWRKRSRQNSQSTCIGTDLNRNF-D 255
QY 203 KHWCEGASSSCSETYCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIFFPYS 262
DB 256 VSWDSSPNTKPCNLVYRGPAPESEKETKAVTNFIRSHLSIKAYITFFHSYQWLLIPYG 315
QY 263 YTRSKSKDHELSLVASEAVRAIEKTSKNTRYTHGSETLYLAPGGDDWIYDLGIKYS 322
DB 316 YTFKLPNHDLLKVIATDAL-STRYETRIYIGPIASTIYKTSGLSDWVYDLGIKHT 374
QY 323 F 323
DB 375 F 375

RESULT 12
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-277-540-7

Query Match 35.2%; Score 632; DB 1; Length 417;
Best Local Similarity 38.2%; Pred. No. 7.4e-61;
Matches 138; Conservative 57; Mismatches 122; Indels 44; Gaps 7;

QY 1 FQSGQVLAALPRTSROVQVQLNLTITTYEIVLWQPVTDALIVKKQVHFFVNASDNDVKA 60
DB 21 FDREKVFVKLQNEKHASVLKNTLSIELDFWYDPAIDHDAVNMVDFRVSEKESQTIQS 80
QY 61 HLNVSIGIPCSVLLADVEDLIQQQIS-NDTVSPRASASYEYQVHSLNEIYSWIEFITERHP 119
DB 81 TLEQHKIHYEILIHDLQEEIEKQDFVKDEIAGRHS---YAKYNDWDKIVSWTEKMLEKHP 137
QY 120 DMLTKIHIGSSFYKLYVVLKVSKEQTAKNAIWDGCIHAREWISPAFCLEWFI----- 173
DB 138 EMVSRIKIGSTVEDNPLYVLKI-GKKGGERKAIFMDCGIHAREWISPAFCQWFVYQATKS 196
QY 174 -GHN-----RMWRKNRSFYANNHCIGTDLNRNFS 202
DB 197 YGKNKIMTKLDRMNFVLPVFNVDGYIWSWTQDRMWRKRSRQNSQSTCIGTDLNRNF-D 255
QY 203 KHWCEGASSSCSETYCGLYPESEPEVKAVASFLRNINQIKAYISMHSYSQHIFFPYS 262
DB 256 VSWDSSPNTKPCNLVYRGPAPESEKETKAVTNFIRSHLSIKAYITFFHSYQWLLIPYG 315
QY 263 YTRSKSKDHELSLVASEAVRAIEKTSKNTRYTHGSETLYLAPGGDDWIYDLGIKYS 322
DB 316 YTFKLPNHDLLKVIATDAL-STRYETRIYIGPIASTIYKTSGLSDWVYDLGIKHT 374
QY 323 F 323
DB 375 F 375

RESULT 13
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
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CLASSIFICATION: 514  
PRIOR APPLICATION DATA: US 08/277,540  
APPLICATION NUMBER: 19-JUL-1994  
FILING DATE: 08/167727  
APPLICATION NUMBER: 15-DEC-1993  
FILING DATE: 07/959944  
APPLICATION NUMBER: 14-OCT-1992  
FILING DATE: 07/649591  
APPLICATION NUMBER: 01-FEB-91  
FILING DATE: ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-7

[illegible]

```

RESULT 14
US-07-649-591B-6
; Sequence 6, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel
; TITLE OF INVENTION: No. 5206161ele
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California

```

COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-649-591B-6

Query Match	34.6%;	Score	622;	DB	1;	Length	417;
Best Local Similarity	35.5%;	Pred.	No. 9.4e-60;				
Matches	128;	Conservative	71;	Mismatches	118;	Indels	44;
Gaps	7;						

  

QY	1	FOSGOVLAALPRTSRQVQLQNLTTTTEIYVLWQPVADLIIVKKQVHFFVNASDSDVNKA	60
DB	21	FOREKVPYRKQDEKQADIIKOLAKTNELDFWPGATHVAANMMVDFRSEKESQAIQS	80
QY	61	HLNVSGIPCSVLADVEDLIIOQIS--NDIVSPRASASYEQYHSLNEIYSWIFETERH	119
DB	81	ALDQNMWYEIILHDLQEEIEKQFDVKEIIPGRHS--YAKYNNWKEIYAWTEKMDKYP	137
QY	120	DMLTKIHIGSSREKYPYLVLYKSGKQTKNAIWDPCGHAREWISAPCLWFI----	173
DB	138	EMWSRIKIGSTVEDNPYLVKI--GEKNEFKALFMDCGIHAREWISAPQWFVQATKT	196
QY	174	-----GH-----NRMRKNRSFYANNHCITGTDLNRNFS	202
DB	197	YGRNKIMTKLLDRMNFYILPVFNVDGYIVSWTKNRMWRKNRSKNQNSKCICTDLNRNF--	255
QY	203	KHWCEBGAASSCSSETYCGLYPESEPEVAVASFLRNINQIKAYISMSHYSQHIYPPYS	262
DB	256	ASWNSIPTNDPCADNYRGSAPESKETAVTNFIHSLNEIKVYITFHSYQMLFFPYG	315
QY	263	YTRSKSKDHEELSLVASEAVRATEKTSKNTYTHGHGSETLYLAPGGDDDWIYDLGIKYS	322
DB	316	YTSKLPNNHDLAKVAKIGTDVL--STRYITRYIYGPIESTIYIPSGSSLDWADYDLGIKHT	374
QY	323	F 323	
DB	375	F 375	

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RESULT 15
US-08-277-540-6
; Sequence 6, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 28, 2004, 19:43:44 ; Search time 77.339 Seconds  
(without alignments)  
1416.943 Million cell updates/sec

Title: US-09-980-881a-3

Perfect score: 1798

Sequence: 1 FOSGQVLAALPRTSRQVQL.....IKYSFTSNPPVEKLLPLSLK 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1717	95.5	386	9	US-09-813-133A-2
2	1717	95.5	386	14	US-10-212-877-2
3	1699.5	94.5	423	14	US-10-379-836-17
4	1688.5	93.9	423	9	US-09-813-133A-4
5	1688.5	93.9	423	14	US-10-212-877-4
6	1676	93.2	428	15	US-10-115-479-68
7	1676	93.2	428	15	US-10-115-479-70
8	1615.5	89.8	423	14	US-10-379-836-2
9	1487.5	82.7	422	14	US-10-379-836-18
10	1466.5	81.6	422	14	US-10-379-836-16
11	1297	72.1	322	15	US-10-115-479-64
12	1258	70.0	354	15	US-10-115-479-66
13	816.5	45.4	211	9	US-09-925-302-467

14	816.5	45.4	211	10	US-09-925-302-467	Sequence 467, App
15	646.5	36.0	416	15	US-10-074-978A-269	Sequence 269, App
16	637.5	35.5	402	14	US-10-379-836-20	Sequence 20, Appl
17	637.5	35.5	417	15	US-10-074-978A-267	Sequence 267, App
18	637.5	35.5	417	15	US-10-074-978A-268	Sequence 268, App
19	637.5	35.5	417	16	US-10-477-515-3	Sequence 3, Appl
20	630.5	35.1	416	15	US-10-074-978A-270	Sequence 270, App
21	622	34.6	417	14	US-10-229-546-2	Sequence 2, Appl
22	622	34.6	417	14	US-10-229-546-9	Sequence 9, Appl
23	622	34.6	417	14	US-10-341-434-188	Sequence 188, App
24	622	34.6	417	15	US-10-262-511-72	Sequence 72, Appl
25	619.5	34.5	716	9	US-09-910-059-125	Sequence 125, App
26	618	34.4	416	15	US-10-074-978A-366	Sequence 266, App
27	612	34.0	434	16	US-10-477-515-2	Sequence 2, Appl
28	612	34.0	437	13	US-10-200-344-10	Sequence 10, Appl
29	612	34.0	437	14	US-10-274-639-12	Sequence 12, Appl
30	612	34.0	437	15	US-10-333-564-12	Sequence 12, Appl
31	610	33.9	437	17	US-10-757-272-128	Sequence 128, App
32	569	31.6	374	9	US-09-888-615-61	Sequence 61, Appl
33	569	31.6	444	14	US-10-176-306-74	Sequence 74, Appl
34	554	30.8	399	14	US-10-200-910-8	Sequence 8, Appl
35	554	30.8	399	17	US-10-843-130-8	Sequence 8, Appl
36	549	30.5	613	9	US-09-910-059-113	Sequence 113, App
37	549	30.5	613	16	US-10-608-710-4	Sequence 4, Appl
38	536.5	29.8	419	15	US-10-072-012-788	Sequence 788, App
39	534.5	29.7	350	13	US-10-200-344-12	Sequence 12, Appl
40	530	29.5	286	15	US-10-072-012-887	Sequence 887, App
41	527.5	29.3	419	15	US-10-257-174-40	Sequence 40, Appl
42	527.5	29.3	436	14	US-10-200-910-6	Sequence 6, Appl
43	527.5	29.3	436	15	US-10-072-012-316	Sequence 316, App
44	527.5	29.3	436	15	US-10-072-012-784	Sequence 784, App
45	527.5	29.3	436	15	US-10-257-174-39	Sequence 39, Appl

## ALIGNMENTS

### RESULT 1

US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 95.5%; Score 1717; DB 9; Length 386;  
Best Local Similarity 99.4%; Pred. No. 7.9e-162;  
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	FOSGQVLAALPRTSRQVQLNTTTEIVLWQPVTTADLIVKKQVHFFVNASDVNDVKA	60
DB	23	FOSGQVLAALPRTSRQVQLNTTTEIVLWQPVTTADLIVKKQVHFFVNASDVNDVKA	82
QY	61	HLNVSIPCSVLLADVEDIQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD	120
DB	83	HLNVSIPCSVLLADVEDIQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD	142
QY	121	MLTKIHGSSPFKPLYLVKVGKQTAKNAIWDGCIHAREWISPAFCLWFIHNRMR	180
DB	143	MLTKIHGSSPFKPLYLVKVGKQTAKNAIWDGCIHAREWISPAFCLWFIHNRMR	202





Qy 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142  
Qy 121 MLTKIHIGSSPEKPYLVLYKVSQKQAKNAIWDGCIHAREWISPAFCLWFIGH----- 175  
Db 143 MLTKIHIGSSPEKPYLVLYKVSQKQAKNAIWDGCIHAREWISPAFCLWFIGHITQFY 202  
Qy 176 -----NRMWRKNSFYANNHCIGTDLNRNFASK 203  
Db 203 GLIGQYTNLLRLVDFYVMPVNVVDGYDSWKCKNRMRKNSFYANNHCIGTDLNRNFASK 262  
Qy 204 HWCBEGASSSCSTYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 263  
Db 263 HWCBEGASSSCSTYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 322  
Qy 264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSF 323  
Db 323 TRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSF 382  
Qy 324 T 324  
Db 383 T 383  
RESULT 5  
US-10-212-877-4  
; Sequence 4, Application US/10212877  
; Publication No.: US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
US-10-212-877-4  
Query Match 93.9%; Score 1688.5; DB 14; Length 423;  
Best Local Similarity 89.2%; Pred. No. 6.2e-159;  
Matches 322; Conservative 0; Mismatches 2; Indels 37; Gaps 1;  
Qy 1 FQSQVLAALPRTSRQVQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDVNVKA 60  
Db 23 FQSQVLAALPRTSRQVQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDVNVKA 82  
Qy 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQVHSLNEIYSWIEFITERHPD 142  
Qy 121 MLTKIHIGSSPEKPYLVLYKVSQKQAKNAIWDGCIHAREWISPAFCLWFIGH----- 175  
Db 143 MLTKIHIGSSPEKPYLVLYKVSQKQAKNAIWDGCIHAREWISPAFCLWFIGHITQFY 202  
Qy 176 -----NRMWRKNSFYANNHCIGTDLNRNFASK 203  
Db 203 GLIGQYTNLLRLVDFYVMPVNVVDGYDSWKCKNRMRKNSFYANNHCIGTDLNRNFASK 262  
Qy 204 HWCBEGASSSCSTYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 263  
Db 263 HWCBEGASSSCSTYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIIVFPYSY 322  
Qy 264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSF 323

Db 323 TRSKSKDHEELSLVASEAVRAIEKISKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSF 382  
Qy 324 T 324  
Db 383 T 383  
RESULT 6  
US-10-115-479-68  
; Sequence 68, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 68  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-68  
Query Match 93.2%; Score 1676; DB 15; Length 428;  
Best Local Similarity 88.0%; Pred. No. 1.1e-157;

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Db	23	FOSQVLAALPRTSRQVQLNLTITTTTVEIVLWQPVTADLI VKKQVHFVNASDVNVKA	82							
Qy	61	HLNVSGIPCSVLLADVDEL IQQQISNDTVSPRASASYEQYHSLNEIYSWTIEFTERHPD	120							
Db	83	HLNVSGIPCSVLLADVDEL IQQQISNDTVSPRASASYEQYHSLNEIYSWTIEFTERHPD	142							
Qy	121	MLTKIHIGSSFEEKYPLVVK-----VSGKEQTAKNAIWDCGIIHAREWISPAFCFLWFIGH	175							
Db	143	MLTKIHIGSSFEEKYPLVVKGFPEQVSGKEQAANKNAIWDCGIIHAREWISPAFCFLWFIGH	202							
Qy	176	-----NRMRKNRSFYANNHCIGTDLNR	198							
Db	203	ITQFYGIIGQYTNLRLLVDFYVPMPVNVVDGYDSWKGNRMWRMKNRSFYANNHCIGTDLNR	262							
Qy	199	NFASKHWCEGASSSSCSETYCGLYPSEPEPVKAVASFLRNNINQIKAYISMHSYSQHIV	258							
Db	263	NFASKHWCEGASSSSCSETYCGLYPSEPEPVKAVASFLRNNINQIKAYISMHSYSQHIV	322							
Qy	259	FPFSYTRSKSDHELSIVASEAVRAETKTSKNTRYTHGHGETLYILAPCGGGDDWIYDLG	318							
Db	323	FPFSYTRSKSDHELSIVASEAVRAETKTSKNTRYTHGHGETLYILAPCGGGDDWIYDLG	382							
Qy	319	IKYSFT 324								
Db	383	IKYSFT 388								

## RESULT 7

US-10-115-479-70  
; Sequence 70, Application US/10115479

; Publication No. US20  
: GENERAL INFORMATION:

APPLICANT:	Li, Li
APPLICANT:	Gerlach, Valerie L.
APPLICANT:	Liu, Xiaohong
APPLICANT:	Miller, Charles E.
APPLICANT:	Spytek, Kimberly A.
APPLICANT:	Zerhusen, Bryan D.
APPLICANT:	Pena, Carol E.A.
APPLICANT:	Shenoy, Suresh G.
APPLICANT:	Zhong, Haihong
APPLICANT:	Smithson, Glendoda
APPLICANT:	Casman, Stacie J.
APPLICANT:	Boldog, Ferenc L.
APPLICANT:	Voss, Edward
APPLICANT:	Vernet, Corine
APPLICANT:	MacDougall, John A.
APPLICANT:	Rastelli, Luca
APPLICANT:	Anderson, David W.
APPLICANT:	Zhong, Mei
APPLICANT:	Mezes, Peter S.
APPLICANT:	Furtak, Katarzyna
APPLICANT:	Patturajan, Meera
APPLICANT:	Burgess, Catherine
APPLICANT:	Malyanker, Uriel M.
APPLICANT:	Shimkets, Richard A.
APPLICANT:	Taupier, Raymond J.
APPLICANT:	Edinger, Shlomit R.

```

, APPLICANT: Mazur, Ann
, TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
, FILE REFERENCE: 21402-322 B (Cura 622 PT)
, CURRENT APPLICATION NUMBER: US10/115,479
, CURRENT FILING DATE: 2002-11-18
, PRIOR APPLICATION NUMBER: 60/281,136
, PRIOR FILING DATE: 2001-04-03
, PRIOR APPLICATION NUMBER: 60/281,863
, PRIOR FILING DATE: 2001-04-05
, PRIOR APPLICATION NUMBER: 60/281,906
, PRIOR FILING DATE: 2001-04-05

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, PRIOR APPLICATION NUMBER: 60/282,934
, PRIOR FILING DATE: 2001-04-10
, PRIOR APPLICATION NUMBER: 60/283,657
, PRIOR FILING DATE: 2001-04-13
, PRIOR APPLICATION NUMBER: 60/283,678
, PRIOR FILING DATE: 2001-04-13
, PRIOR APPLICATION NUMBER: 60/283,687
, PRIOR FILING DATE: 2001-04-13
, PRIOR APPLICATION NUMBER: 60/283,710
, PRIOR FILING DATE: 2001-04-13
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, PRIOR FILING DATE: 2001-04-17
, PRIOR APPLICATION NUMBER: 60/285,325
, PRIOR FILING DATE: 2001-04-19
, Remaining Prior Application data removed - See File Wrapper or PALM.
, NUMBER OF SEQ ID NOS: 198
, SEQ ID NO 70
, LENGTH: 428
, TYPE: PRT
, ORGANISM: Homo sapiens
, US-10-115-479-70

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Query Match 93.2%; Score 1676; DB 15; Length 428;  
Best Local Similarity 88.0%; Pred. No. 1.1e-157;  
Matches 322; Conservative 0; Mismatches 2; Indels 42

Qy	1	FQSQVLAALPRTSRQVQVLONLTTTVEIYVLWQVPTADLIYVKKQVHFVFNASDVNDVKA	60
Db	23	FQSQVLAALPRTSRQVQVLONLTTTVEIYVLWQVPTADLIYVKKQVHFVFNASDVNDVKA	82
Qy	61	HLNVSGIPCSVLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD	120
Db	83	HLNVSGIPCSVLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD	142
Qy	121	MLTKIHGSSFEKYPYLVLK-----VSGIEQTAKNAIWDGCIHAREWISPAFCLEWIGH	175
Db	143	MLTKIHGSSFEKYPYLVLAGFPEQVSGIEQAAKNAIWDGCIHAREWISPAFCLEWIGH	202
Qy	176	-----NRMRKQSRFYANNHCIGTDLNR	198
Db	203	ITQPYGIGQVTNLLRLRVDFYMPVNVUIGDYDSWKKNRMRKSRFYANNHCIGTDLNR	262
Qy	199	NFASKHWCBGASSSCSEYTCGLYPESIPEVKAVASFLRNNINOIKAYISMHSYSOHIV	258
Db	263	NFASKHWCBGASSSCSEYTCGLYPESIPEVKAVASFLRNNINOIKAYISMHSYSOHIV	322
Qy	259	FPFSYTRSKDKHHEELSLVASEAVRAIEITSKNTRYTHGHGSETLYLAPCGGDDWIYDLG	318
Db	323	FPFSYTRSKDKHHEELSLVASEAVRAIEITSKNTRYTHGHGSETLYLAPCGGDDWIYDLG	382
Qy	319	IKYSFT 324	
Db	383	IKYSFT 388	

RESULT 8

U.S.-10-379-836-2

0010393020 ; Sequence 2, Application US/10379836  
0010393020 ; Publication No. US20030215850A1

GENERAL INFORMATION:

```

/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID
/ TITLE OF INVENTION: TAFI
/ FILE REFERENCE: D0214NP
/ CURRENT APPLICATION NUMBER: US/10/379,8
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: U.S. 60/361,5
/ PRIOR FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 423
/ TYPE: PRT
/

```

ORGANISM: Papio hamadryas  
US-10-379-836-2

Query Match 89.8%; Score 1615.5; DB 14; Length 423;

Best Local Similarity 85.0%; Pred. No. 1.1e-151;  
Matches 307; Conservative 8; Mismatches 9; Indels 37; Gaps 1;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 60  
DB 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGH----- 175  
DB 143 MLTKIHIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGHTEYY 202  
QY 176 -----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
DB 203 GIIGEYTNLLRHVDIFYMPVNVVDGYDSWKKNRMWRKNRSFYANNRCIGTDLNRNFASK 262  
QY 204 HWCCEGASSSCSETYCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQIHVFPYSY 263  
DB 263 HWCCEGASSSCSETYCGLYPSEPEVKAVANFLRRNINHIKAYISMHSYSQIHVFPYSY 322  
QY 264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 323  
DB 323 TRSKSKDHEELSLVASEAVRAIOKTSKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 382  
QY 324 T 324  
DB 383 T 383

## RESULT 9

US-10-379-836-18

; Sequence 18, Application US/10379836  
; Publication No. US20030215850A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON

; FILE REFERENCE: D0214NP

; CURRENT APPLICATION NUMBER: US/10/379,836

; PRIOR FILING DATE: 2003-03-04

; PRIOR FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 18

; LENGTH: 422

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-379-836-18

Query Match

Best Local Similarity 82.7%; Score 1487.5; DB 14; Length 422;

Matches 282; Conservative 20; Mismatches 22; Indels 37; Gaps 1;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 60  
DB 22 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 81  
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
DB 82 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 141  
QY 121 MLTKIHIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGH----- 175  
DB 142 MLTKIHIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGHTEYY 201

QY 176 -----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
DB 202 GKENTYTNLLRHVDIFYMPVNVVDGYDTWKKNRMWRKNRSFYANNRCIGTDLNRNFASK 261  
QY 204 HWCCEGASSSCSETYCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQIHVFPYSY 263  
DB 262 HWCCEGASSSCSETYCGLYPSEPEVKAVADFLRRNINHIKAYISMHSYSQOILFPYSY 321  
QY 264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 323  
DB 322 NRKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 381  
QY 324 T 324  
DB 382 T 382

## RESULT 10

US-10-379-836-16

; Sequence 16, Application US/10379836

; Publication No. US20030215850A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON

; FILE REFERENCE: D0214NP

; CURRENT APPLICATION NUMBER: US/10/379,836

; PRIOR FILING DATE: 2003-03-04

; PRIOR FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 422

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-379-836-16

Query Match

Best Local Similarity 81.6%; Score 1466.5; DB 14; Length 422;

Matches 277; Conservative 22; Mismatches 25; Indels 37; Gaps 1;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 60  
DB 22 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVFNASDVNDVKA 81  
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
DB 82 YLNASRIPEFNVLMNNVEDLIQQOISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 141  
QY 121 MLTKIHIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGH----- 175  
DB 142 MLQKIYIGSSFEKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIQGHTEYY 201  
QY 176 -----NRMWRKNRSFYANNHCIGTDLNRNFASK 203  
DB 202 GKENTYTNLLRHVDIFYMPVNVVDGYDTWKKNRMWRKNRSFYANNRCIGTDLNRNFASK 261  
QY 204 HWCCEGASSSCSETYCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSQIHVFPYSY 263  
DB 262 HWCCEGASSSCSETYCGLYPSEPEVKAVADFLRRNINHIKAYISMHSYSQOILFPYSY 321  
QY 264 TRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 323  
DB 322 NRKSKDHEELSLVASEAVRAIESINKNTRYTHGSGSETLYLAPGGDDMIYDLGIKYSF 381  
QY 324 T 324  
DB 382 T 382

## RESULT 11

US-10-115-479-64

; Sequence 64, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 64  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-64

Query Match 72.1%; Score 1297; DB 15; Length 322;  
Best Local Similarity 79.6%; Pred. No. 3.7e-120;  
Matches 258; Conservative 0; Mismatches 2; Indels 64; Gaps 1;

Qy 1 FQSGVLAALPRTSRQVQLNLTFTTVEIWLQVPTADLIYKKQVHFFVFNASVDNVKA 60  
Db 23 FQSGVLAALPRTSRQVQLNLTFTTVEIWLQVPTADLIYKKQVHFFVFNASVDNVKA 82  
Qy 61 HLNVSIGPCSVLLADVEDLIQQQLSNDTVSPRASAYVEQVHSLNELYSWIEFTTERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQQLSNDTVSPRASAYVEQVHSLNELYSWIEFTTERHPD 142

Qy 121 MLTKIHGSGFEKYPYLVKVGKQTAAYNAIWDCGIHAREWISPAFCLWFIHGNMWR 180  
Db 143 MLTKIHGSGFEKYPYLVKVGKQTAAYNAIWDCGIHAREWISPAFCLWFIHGNMWR 177  
Qy 181 KNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRN 240  
Db 178 -----CGLYPESEPEVKAVASFLRN 198  
Qy 241 INQIKAYISMHSYSHIVFPYSYTRSKSDHELSLVASEAVRAIKTSKNTRYTHGHGS 300  
Db 199 INQIKAYISMHSYSHIVFPYSYTRSKSDHELSLVASEAVRAIKTSKNTRYTHGHGS 258  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFT 324  
Db 259 ETLYLAPGGDDWIYDLGIKYSFT 282

RESULT 12  
US-10-115-479-66  
; Sequence 66, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325

; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match 70.0%; Score 1258; DB 15; Length 354;
Best Local Similarity 68.0%; Pred. No. 3.2e-116;
Matches 249; Conservative 0; Mismatches 1; Indels 116; Gaps 3;

QY 1 FQSQVLAALPRTSRQVQLQLNTTYYEIVLWQPVTDADLVKKQVHFFVNASDNDVKA 60
DB 23 FQSQVLAALPRTSRQVQLQLNTTYYEIVLWQPVTDADLVKKQVHFFVNASDNDVKA 82
QY 61 HLNVSIGPCSVLLADVEDLIQQISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 120
DB 83 HLNVSIGPCSVLLADVEDLIQQISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 142
QY 121 MLTKIHIGSSFEXKPLVVK-----VSGKQTAKNAIWDICGHAREWISPAFLWFIH 175
DB 143 MLTKIHIGSSFEXKPLVYKGFQVSGKQAQNAIWDICGHAREWISPAFLWFIH 202
QY 176 -----NRMWRKNRSFYANNHCIGTDLNR 198
DB 203 ITQFYGIIGQYTNLLRLVDFVMPVNVVDGYDSWKKNRMWRKNRSFYANNHCIGTDLNR 262
QY 199 NFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIV 258
DB 263 NFASKHWCBEAGSSSCSETYCGLYPE----- 289
QY 259 FPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHSETLYLAPCGGDDWIYDLG 318
DB 290 -----SETLYLAPCGGDDWIYDLG 308
QY 319 IKYSFT 324
DB 309 IKYSFT 314

RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match 45.4%; Score 816.5; DB 9; Length 211;
Best Local Similarity 90.6%; Pred. No. 1.3e-72;
Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 163 WISPAFLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 214
DB 3 WIS-MLCRLWLMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 61
QY 215 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
DB 62 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Query Match 45.4%; Score 816.5; DB 9; Length 211;
Best Local Similarity 90.6%; Pred. No. 1.3e-72;
Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 163 WISPAFLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 214
DB 3 WIS-MLCRLWLMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 61
QY 215 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
DB 62 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

; CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121
; SLVASEAVRAIEKTSKNTRYTHGHSETLYLAPCGGDDWIYDLGIKYSFT 324
; SLVASEAVRAIEKTSKNTRYTHGHSETLYLAPCGGDDWIYDLGIKYSFT 171

RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match 45.4%; Score 816.5; DB 10; Length 211;
Best Local Similarity 90.6%; Pred. No. 1.3e-72;
Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 163 WISPAFLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 214
DB 3 WIS-MLCRLWLMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 61
QY 215 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
DB 62 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121

Query Match 45.4%; Score 816.5; DB 10; Length 211;
Best Local Similarity 90.6%; Pred. No. 1.3e-72;
Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 163 WISPAFLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 214
DB 3 WIS-MLCRLWLMVMNYSWKKNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCBEAGSSSS 61
QY 215 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 274
DB 62 CSETYCGLYPESPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSYTRSKSKDHEEL 121



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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:35:31 ; Search time 312.936 Seconds  
(without alignments)  
1196.740 Million cell updates/sec

Title: US-09-980-881A-3

Perfect score: 1798

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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3: /cgn2\_6/ptodata/1/paa/US07 COMB.pcp.\*

4: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*

5: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*

6: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*

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24: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

25: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

26: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

27: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

28: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

29: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

30: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

31: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

32: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

33: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

34: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

35: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

36: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Query Match

100.0%; Score 1798; DB 25; Length 338;

Result No.	Score	Query Match	Length	DB	ID	Description
1	1798	100.0	338	25	US-09-980-881-3	Sequence 3, Appli
2	1798	100.0	338	25	US-09-980-881A-3	Sequence 3, Appli
3	1786	99.3	360	27	US-10-170-205E-13306	Sequence 13306, A
4	1786	99.3	360	34	US-10-803-180-126	Sequence 126, App
5	1786	99.3	360	35	US-10-918-754-1941	Sequence 1941, Ap
6	1786	99.3	360	36	US-60-452-680-21530	Sequence 21530, A
7	1786	99.3	360	36	US-60-453-050-13037	Sequence 13037, A
8	1786	99.3	360	36	US-60-453-135-13037	Sequence 13037, A
9	1786	99.3	360	36	US-60-455-444-6989	Sequence 6989, Ap
10	1786	99.3	360	36	US-60-465-241-6989	Sequence 6989, Ap
11	1786	99.3	360	36	US-60-466-412-13037	Sequence 13037, A
12	1786	99.3	360	36	US-60-495-114-1941	Sequence 1941, Ap
13	1786	99.3	366	24	US-09-949-003C-3190	Sequence 3190, Ap
14	1786	99.3	366	24	US-09-949-003C-3191	Sequence 3191, Ap
15	1785	99.3	360	25	US-09-980-881-2	Sequence 2, Appli
16	1785	99.3	360	25	US-09-980-881A-2	Sequence 2, Appli
17	1784	99.2	360	22	US-09-791-537-142876	Sequence 142876, A
18	1784	99.2	360	24	US-09-949-003C-2616	Sequence 2616, Ap
19	1718	95.6	386	1	PCT-US03-31531-18	Sequence 18, Appli
20	1717	95.5	386	1	PCT-US02-08289-2	Sequence 2, Appli
21	1717	95.5	386	28	US-10-212-877-2	Sequence 2, Appli
22	1699.5	94.5	423	1	PCT-US03-26773-2	Sequence 3, Appli
23	1699.5	94.5	423	3	US-07-959-944A-3	Sequence 96834, A
24	1699.5	94.5	423	22	US-09-791-537-96834	Sequence 2062, Ap
25	1699.5	94.5	423	24	US-09-949-003C-2062	Sequence 17, Appli
26	1699.5	94.5	423	29	US-10-379-836-17	Sequence 2, Appli
27	1699.5	94.5	423	30	US-10-486-034-2	Sequence 3726, Ap
28	1699.5	94.5	423	36	US-60-353-790-3726	Sequence 17, Appli
29	1699.5	94.5	423	36	US-60-361-523-17	Sequence 13305, A
30	1694.5	94.2	423	37	US-10-170-205E-13305	Sequence 127, App
31	1694.5	94.2	423	34	US-10-803-180-127	Sequence 1942, Ap
32	1694.5	94.2	423	35	US-10-918-754-1942	Sequence 21529, A
33	1694.5	94.2	423	36	US-60-452-680-21529	Sequence 13036, A
34	1694.5	94.2	423	36	US-60-453-050-13036	Sequence 13036, A
35	1694.5	94.2	423	36	US-60-453-135-13036	Sequence 6988, Ap
36	1694.5	94.2	423	36	US-60-455-444-6988	Sequence 6988, Ap
37	1694.5	94.2	423	36	US-60-465-241-6988	Sequence 13036, A
38	1694.5	94.2	423	36	US-60-466-412-13036	Sequence 1942, Ap
39	1694.5	94.2	423	36	US-60-495-114-1942	Sequence 1824, Ap
40	1694.5	94.2	424	22	US-09-760-475-1824	Sequence 1824, Ap
41	1694.5	94.2	424	28	US-10-227-425-1824	Sequence 3188, Ap
42	1694.5	94.2	429	24	US-09-949-003C-3188	Sequence 3189, Ap
43	1688.5	93.9	423	1	PCT-US02-08289-4	Sequence 4, Appli
44	1688.5	93.9	423	28	US-10-212-877-4	Sequence 4, Appli
45	1688.5	93.9	423	28	US-10-212-877-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-980-881-3

; Sequence 3, Application US/09980881

; GENERAL INFORMATION:

; APPLICANT: AKIRA MATSUMOTO

; TITLE OF INVENTION: Human Brain Carboxypeptidase B

; FILE REFERENCE: MAT-101PCT

; CURRENT APPLICATION NUMBER: US/09/980,881

; CURRENT FILING DATE: 2001-10-30

; PRIOR APPLICATION NUMBER: JP 1999-125169

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 338

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-980-881-3

Best Local Similarity 100.0%; Pred. No. 4.3e-182; Mismatches 0; Indels 0; Gaps 0;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60  
Db 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60

Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120

Qy 121 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 180  
Db 121 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 180

Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 240

Qy 241 INQIKAYISMHSYSHQIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 241 INQIKAYISMHSYSHQIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300

Qy 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338

RESULT 2  
US-09-980-881a-3  
; Sequence 3, Application US/09980881a  
; GENERAL INFORMATION:  
; APPLICANT: AKIRA MATSUMOTO  
; TITLE OF INVENTION: Human Brain Carboxypeptidase B  
; FILE REFERENCE: MAT-101PCT  
; CURRENT APPLICATION NUMBER: US/09/980.881a  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: JP 1999-125169  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-980-881a-3

Query Match 100.0%; Score 1798; DB 25; Length 338;  
Best Local Similarity 100.0%; Pred. No. 4.3e-182;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60  
Db 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60

Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120

Qy 121 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 180  
Db 121 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 180

Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 240

Qy 241 INQIKAYISMHSYSHQIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 241 INQIKAYISMHSYSHQIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300

Qy 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338

Db 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338

RESULT 3  
US-10-170-205E-13306  
; Sequence 13306, Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF  
; FILE REFERENCE: CL001381  
; CURRENT APPLICATION NUMBER: US/10/170,205E  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13306  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205E-13306

Query Match 99.3%; Score 1786; DB 27; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60  
Db 23 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 142

Qy 121 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 180  
Db 143 MLTKIHIGSSPEKPYLVKVSQGEQAKNAIWDGHHAREWISPAFCFLWFIHGNRMWR 202

Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGSSSSCSETYCGLYPESEPEVKAVASFLRRN 262

Qy 241 INQIKAYISMHSYSHQIVFPYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSHQIVFPYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322

Qy 301 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLVLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 4  
US-10-803-180-126  
; Sequence 126, Application US/10803180  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001511  
; CURRENT APPLICATION NUMBER: US/10/803,180  
; CURRENT FILING DATE: 2004-03-18  
; NUMBER OF SEQ ID NOS: 6676  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 126  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-803-180-126

Query Match 99.3%; Score 1786; DB 34; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGVLAALPRTSRQVQLNLTITTYEIVLWQVPTADLVKKQVHFFVNASDNDVKA 60



Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 82  
Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 142  
Qy 121 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 180  
Db 143 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 202  
Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 262  
Qy 241 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 5  
US-10-918-754-1941  
; Sequence 1941, Application US/10918754  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND  
; FILE REFERENCE: CL001480  
; CURRENT APPLICATION NUMBER: US/10/918,754  
; CURRENT FILING DATE: 2004-08-16  
; NUMBER OF SEQ ID NOS: 91238  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1941  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-918-754-1941

Query Match 99.3%; Score 1786; DB 35; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 82  
Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 142  
Qy 121 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 180  
Db 143 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 202  
Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 262  
Qy 241 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 6

US-60-452-680-21530  
; Sequence 21530, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001450  
; CURRENT APPLICATION NUMBER: US/60/452,680  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 116213  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21530  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-452-680-21530

Query Match 99.3%; Score 1786; DB 36; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 82  
Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASASYEQVHSLNEIYSWIEFTTERHPD 142  
Qy 121 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 180  
Db 143 MLTKIHIGSSPEKYPYLVVYKVSQKEQAKNAIWDGCIHAREWISPAFLWFIHGNRMWR 202  
Qy 181 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESPEVKAVASFLRRN 262  
Qy 241 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSHQIVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 7  
US-60-453-050-13037  
; Sequence 13037, Application US/60453050  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001457  
; CURRENT APPLICATION NUMBER: US/60/453,050  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13037  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-453-050-13037

Query Match 99.3%; Score 1786; DB 36; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIQLWQVPTADLIIVKKQVHFFVNASDNDVKA 82

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QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 120
DB 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 142
QY 121 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 180
DB 143 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 202
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 240
DB 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 262
QY 241 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
DB 263 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322
QY 301 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 338
DB 323 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 360

RESULT 8
US-60-453-135-13037
; Sequence 13037, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; NUMBER OF SEQ ID NOS: 2003-03-10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13037
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13037

Query Match 99.3%; Score 1786; DB 36; Length 360;
Best Local Similarity 99.4%; Pred. No. 9.1e-181;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 60
DB 23 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 82
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 120
DB 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 142
QY 121 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 180
DB 143 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 202
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 240
DB 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 262
QY 241 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
DB 263 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322
QY 301 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 338
DB 323 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 360

RESULT 9
US-60-455-444-6989
; Sequence 6989, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; NUMBER OF SEQ ID NOS: 2003-03-18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-6989

Query Match 99.3%; Score 1786; DB 36; Length 360;
Best Local Similarity 99.4%; Pred. No. 9.1e-181;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 60
DB 23 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 82
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 120
DB 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 142
QY 121 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 180
DB 143 MLTKIHIGSSPEKPYLYLVKVSKEQAKNAIWDGCIHAREWISPAFCFLWFIHGNMWR 202
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 240
DB 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRNN 262
QY 241 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300
DB 263 INQIKAYISMHSYQHVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322
QY 301 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 338
DB 323 ETLYLAPGGDDWYDYGKYSFTSNPPVEKLLPLSLK 360

RESULT 10
US-60-465-241-6989
; Sequence 6989, Application US/60465241
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001468
; CURRENT APPLICATION NUMBER: US/60/465,241
; NUMBER OF SEQ ID NOS: 258418
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6989
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-465-241-6989

Query Match 99.3%; Score 1786; DB 36; Length 360;
Best Local Similarity 99.4%; Pred. No. 9.1e-181;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 60
DB 23 FQSGQVLAALPRTSRQVQLQNLTTTYEIVLWQPVTDALIVKKQVHFFVNASDNDNVKA 82
QY 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYVEQYHSLNEIYSWIEFITERHPD 120
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Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIHNRMR 180  
Db 143 MLTKIHIGSSFEPKYPVLYLVKVSKEQAANKNAIWDGCIHAREWISPAFCLWFIHNRMR 202  
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 262  
QY 241 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
QY 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 11  
US-60-466-412-13037  
; Sequence 13037, Application US/60466412  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001466  
; CURRENT APPLICATION NUMBER: US/60/466,412  
; NUMBER OF SEQ ID NOS: 203-04-30  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 13037  
; LENGTH: 360  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
US-60-466-412-13037

Query Match 99.3%; Score 1786; DB 36; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 60  
Db 23 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIHNRMR 180  
Db 143 MLTKIHIGSSFEPKYPVLYLVKVSKEQAANKNAIWDGCIHAREWISPAFCLWFIHNRMR 202  
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 262  
QY 241 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
QY 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 12  
US-60-495-114-1941  
; Sequence 1941, Application US/60495114  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND  
; FILE REFERENCE: CL001480  
; CURRENT APPLICATION NUMBER: US/60/495,114  
; CURRENT FILING DATE: 2003-08-15  
; NUMBER OF SEQ ID NOS: 91238  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 1941  
; LENGTH: 360  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
US-60-495-114-1941

Query Match 99.3%; Score 1786; DB 36; Length 360;  
Best Local Similarity 99.4%; Pred. No. 9.1e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 60  
Db 23 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKYPVLYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIHNRMR 180  
Db 143 MLTKIHIGSSFEPKYPVLYLVKVSKEQAANKNAIWDGCIHAREWISPAFCLWFIHNRMR 202  
QY 181 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFASKHWCCEGASSSSCSETYCGLYPESPEVKAVASFLRRN 262  
QY 241 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSQHIYVFPYSTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 322  
QY 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

RESULT 13  
US-09-949-003C-3190  
; Sequence 3190, Application US/09949003C  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC  
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL000791  
; CURRENT APPLICATION NUMBER: US/09/949,003C  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,446  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 74065  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3190  
; LENGTH: 366  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
US-09-949-003C-3190

Query Match 99.3%; Score 1786; DB 24; Length 366;  
Best Local Similarity 99.4%; Pred. No. 9.4e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 60  
Db 29 FOSGQVLAALPRTSRQVQLQNLTITTYEIVLWQPVTADLIVKKQVHFFVFNASDVNDVKA 88  
QY 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120

Db 89 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 148  
Qy 121 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 180  
Db 149 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 208  
Qy 181 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 209 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 268  
Qy 241 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 269 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 328  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 329 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 366

RESULT 14  
US-09-949-003C-3191  
; Sequence 3191, Application US/09949003C  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC  
; TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO00791  
; CURRENT APPLICATION NUMBER: US/09/949,003C  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,446  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 74065  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3191  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-949-003C-3191

Query Match : 99.3%; Score 1786; DB 24; Length 366;  
Best Local Similarity 99.4%; Pred. No. 9.4e-181;  
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTYYEIVLWQPVTDLIIVKKQVHFFVNASDNDVKA 60  
Db 29 FQSGQVLAALPRTSRQVQLQNLTYYEIVLWQPVTDLIIVKKQVHFFVNASDNDVKA 88  
Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 120  
Db 89 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 148  
Qy 121 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 180  
Db 149 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 208  
Qy 181 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 209 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 268  
Qy 241 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 269 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 328  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 329 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 366

RESULT 15  
US-09-980-881-2  
; Sequence 2, Application US/09980881  
; GENERAL INFORMATION:  
; APPLICANT: AKIRA MATSUMOTO

; TITLE OF INVENTION: Human Brain Carboxypeptidase B  
; FILE REFERENCE: NAT-101PCT  
; CURRENT APPLICATION NUMBER: US/09/980,881  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: JP 1999-125169  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-980-881-2

Query Match : 99.3%; Score 1785; DB 25; Length 360;  
Best Local Similarity 99.1%; Pred. No. 1.2e-180;  
Matches 335; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTYYEIVLWQPVTDLIIVKKQVHFFVNASDNDVKA 60  
Db 23 FQSGQVLAALPRTSRQVQLQNLTYYEIVLWQPVTDLIIVKKQVHFFVNASDNDVKA 82  
Qy 61 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 120  
Db 83 HLNVSIGPCSVLLADVEDLIQQOISNDTVSPRASAYEQYHSLNEIYSWIEFITERHPD 142  
Qy 121 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 180  
Db 143 MLTKIHGSSPEKPYLVLVKVSKEQAKNAIWDGHIHAREWISPAFCLWFIGHNRMWR 202  
Qy 181 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 240  
Db 203 KNRSFYANNHCIGTDLNRNFKSWCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 262  
Qy 241 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 300  
Db 263 INQIKAYISMHSYSQHIHVPFYSYTRSKSDHEELSLVASEAVRAIDKTSKNTRYTHGHGS 322  
Qy 301 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 338  
Db 323 ETLYLAPGGDDWIYDLGIKYSFTSNPPVEKLLPLSLK 360

Search completed: October 28, 2004, 20:01:44  
Job time : 313.936 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 03:40:54 ; Search time 98.464 Seconds  
(without alignments)  
2439.944 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 1798  
Sequence: 1 FOSGQVLAALPRTSRQVQL.....IKYFTSPNPVKKLLPLSLK 338

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 824507 seqs, 35539441 residues  
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO\_spool/US0980881/runat\_28102004\_131642\_12077/app\_query.fasta\_1.1429  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1749.5	97.3	1625	4	US-09-813-133A-1
2	1732	96.3	1272	2	US-08-869-057-1
3	1732	96.3	1749	1	US-07-649-591B-2
4	1732	96.3	1749	1	US-08-277-540-2
5	1732	96.3	1749	1	US-08-430-787A-2
6	646.5	36.0	1215	1	US-08-696-139-1
7	637.5	35.5	1263	2	US-08-860-882A-56
8	637.5	35.5	1263	4	US-09-011-769A-38
9	637.5	35.5	1284	2	US-08-860-882A-71
10	637.5	35.5	1284	4	US-09-011-769A-55
11	622	34.6	1622	4	US-09-023-655-1020
12	619.5	34.5	1311	4	US-09-675-305-9

13	619.5	34.5	1311	4	US-10-200-344-9	Sequence 9, Appli
14	619.5	34.5	2154	3	US-09-171-945-124	Sequence 124, App
15	610	33.9	927	2	US-08-782-760-5	Sequence 5, Appli
16	610	33.9	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	582	32.4	921	1	US-08-696-139-3	Sequence 3, Appli
18	571.5	31.8	2128	4	US-09-675-305-13	Sequence 13, Appli
19	571.5	31.8	2128	4	US-10-200-344-13	Sequence 13, Appli
20	567	31.5	999	2	US-08-860-882A-67	Sequence 67, Appli
21	567	31.5	999	4	US-09-011-769A-50	Sequence 50, Appli
22	567	31.5	1053	2	US-08-860-882A-64	Sequence 64, Appli
23	567	31.5	1053	4	US-09-011-769A-46	Sequence 46, Appli
24	560	31.1	1053	4	US-09-463-451-27	Sequence 27, Appli
25	560	31.1	1053	4	US-09-463-451-28	Sequence 28, Appli
26	560	31.1	1059	2	US-08-860-882A-74	Sequence 74, Appli
27	560	31.1	1059	4	US-09-011-769A-59	Sequence 59, Appli
28	559	31.1	1059	2	US-08-860-882A-77	Sequence 77, Appli
29	559	31.1	1059	4	US-09-011-769A-63	Sequence 63, Appli
30	554	30.8	1200	4	US-09-710-099-7	Sequence 7, Appli
31	554	30.8	1200	4	US-10-200-910-7	Sequence 7, Appli
32	549	30.5	1870	3	US-09-171-945-112	Sequence 112, App
33	534.5	29.7	1050	4	US-10-200-344-11	Sequence 11, Appli
34	534.5	29.7	1050	4	US-09-710-099-5	Sequence 5, Appli
35	527.5	29.3	1311	4	US-10-200-910-5	Sequence 5, Appli
36	527.5	29.3	1311	4	US-08-640-906-3	Sequence 3, Appli
37	516.5	28.7	1251	3	US-09-395-936-3	Sequence 1, Appli
38	516.5	28.7	1251	3	US-08-640-906-1	Sequence 1, Appli
39	491.5	27.3	1257	3	US-09-395-936-1	Sequence 1, Appli
40	491.5	27.3	1257	3	US-09-710-099-3	Sequence 3, Appli
41	467.5	26.0	945	4	US-09-710-099-11	Sequence 11, Appli
42	467.5	26.0	945	4	US-10-200-910-3	Sequence 3, Appli
43	467.5	26.0	945	4	US-10-200-910-11	Sequence 11, Appli
44	467.5	26.0	945	4	US-09-710-099-15	Sequence 15, Appli
45	465.5	25.9	2247	4	US-09-710-099-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:					Pred. No.:	3,19e-215	Length:	1625
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Percent Similarity:					Percent Similarity:	94.38%	Conservative:	0
Best Local Similarity:					Best Local Similarity:	94.38%	Mismatches:	2
Query Match:					Query Match:	97.30%	Indels:	18
DB:					DB:	4	Gaps:	1
US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)								
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Db	83	TTTCAGATGGCCAGCTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA	142					
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Db 143 CAGAACTTACTACACATATGAGATGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 202  
Qy 41 VallyslystysGlnValHisPheValAsnAlaSerAspValAspAsnVallyleAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATGTGATGTCGCAATGTGAAAGCC 262  
Qy 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
Db 263 CATTTAAATGTGACGGAAATTCATGTGAGTGTCTTGTGGCAGATGTGGAAGATCTTATT 322  
Qy 81 GlnGlnGlnLeuSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCAACGACACAGTACGCCCCCGAGCTCCGATCGTACTATGAACAG 382  
Qy 101 TyrHisSerLeuAsnGluileTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAAATGAATCTATTCTTGGATGAATTTATATACTGAGAGCATCCTGAT 442  
Qy 121 MetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrValLeuIys 140  
Db 443 ATGCTTACAAAAATCCACATTTGGATCTCTCAATTTGAGAAGTACCCCACTCTATGTTTAAAG 502  
Qy 141 ValSerGlyIysGluGlnThrAlaIysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTCTGGAAAGAACAGACGACGCAAAATGCCATATGGATTGACTGTGGNATCCATGCC 562  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 563 AGAAGATGGATCT 622  
Qy 181 LysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGTCTCTTCTATGCAACAAATCATTTGCAATCGAACAGACCTGAATAGGAATTT 682  
Qy 201 AlaSerIysHisTrpCysGluGluGluValaSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGGTGTGAGAGAGTGATCCAGTTCCTCATGCTCGAAACCTACTGT 742  
Qy 221 GlyLeuTyrProGluSerGluProGluVallylsAlaValaSerPheLeuArgArgAsn 240  
Db 743 GGACTTTATCTGAGTCAGAACACAGAGTGAAGCAGTGGCTAGTCTTCTTGAGAAGAAAT 802  
Qy 241 IleAsnGlnIleIysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACAGATTAAGCATATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCCTCA 862  
Qy 261 TyrSerTyrThrArgSerIysSerIysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCCTATACAGAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTACCCAGTGAA 922  
Qy 281 AlaValArgAlaIleGluLeuThrSerIysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCGTGTATTGAGAAATTTAGTAAAAATACCAGGTATACATACATGGCCATGGCTCA 982  
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleIys 320  
Db 983 GAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTTGATGATTTGGGCATCAAA 1042  
Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCGTTTACAATTGAATCTCGAGATACGGGCACATACGATTCCTGCTCCGGAGCGT 1102  
Qy 324 -ThrSerAsnProValGluIysLeuLeuProLeuSerLeuIys 338  
Db 1103 TACATCAAAACCCACTGTAGAGAAGCTTTTCCCGCTGTCTCTAAAA 1148

## RESULT 2

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko

; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Lega. Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P.  
; AUTHORS: Henzel, William  
; AUTHORS: Drayna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
; TITLE: from Human Plasma  
; JOURNAL: J. Biol. Chem.  
; VOLUME: 266  
; ISSUE: 32  
; PAGES: 21833-21838  
; DATE: No. 5985562 15-1991  
; US-08-869-057-1  
  
Alignment Scores:  
Pred. No.: 3.8e-213 Length: 1272  
Score: 1732.00 Matches: 338  
Percent Similarity: 86.01% Conservative: 0  
Best Local Similarity: 86.01% Mismatches: 0  
Query Match: 96.33% Indels: 55  
DB: 2 Gaps: 2  
  
US-09-980-881A-3 (1-338) x US-08-869-057-1 (1-1272)  
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 67 TTTTCAGAGTGGCCAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 126  
Qy 21 GlnAsnLeuThrThrThrTyrGluileValLeuTrpGlnProValThrAlaAspLeuile 40  
Db 127 CAGAATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAAACAGCTGACCTTATT 186  
Qy 41 VallyslystysGlnValHisPheValAsnAlaSerAspValAspAsnVallyleAla 60  
Db 187 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATGTGTCGCAATGTGAAAGCC 246  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80

Db 247 CATTAATAATGACCGGAATTCATGACAGTGTCTTGTCGACAGCTGGAAGATCTTTAT 306  
Qy 81 GlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 307 CAACAGCAGATTTCCACGACAGTCAAGCCCGACCTCCGGATCGTACTATGAACAG 366  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 367 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGGCATCTCTGAT 426  
Qy 121 MetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrValLeuLys 140  
Db 427 ATGCTTACAAAATCCCATGATGCTCAATTTGAGAAGTACCACCTCTATGTTTTAAAG 486  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 487 GTTCTGGAAGAAGACAAACAGCCAAATGCCATATGGATGGACTGTGGATCCATGCC 546  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175  
Db 547 AGAAGATGGATCTCTCCTGCTTCTGCTTGTGGTTTCATAGGCCATATAAACAATCTAT 606  
Qy 175 ----- 175  
Db 607 GGATAATAGGGCAATATACCAATCTCTGAGGCTTGCGATTTCTATGTTATGCCGGTG 666  
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
Db 667 GTTAATGTGACGGTTATGACTACTCTAGTGAAGAAAGAAATCGAATGGAGAAGAACCGT 726  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 727 TCTTTCTATCGAACAATCATTTGTCATCGAAGACCTGAATAGGAACCTTGTCTCCAAA 786  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 787 CACTGGTGTGAGGAAGGTGATCCAGTCTCTCATGCTCGGAAACCTACTGTGGACTTTAT 846  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 847 CTTGAGTCAGAACAGAAAGTGAGGAGAGTGGTAGTTCTTGAGAAGAAATATCAACCAG 906  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 907 ATTAAGCATACATCAGCATGCTTCTACTCCAGCATATAGTGTTCATATTCCTAT 966  
Qy 264 ThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 967 ACACGAAGTAAAGCAAGAACCAATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 1026  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1027 GCTATTGAGAAACTAGTAAATAATACAGGTATACATGCGCATGGCTCGAAACCTTA 1086  
Qy 304 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1087 TACTAGCTCTCGAGGTGGGAGCATTTGGATCTATGATTTGGCATCAATATTCGTTT 1146  
Qy 324 -----ThrSerAs 326  
Db 1147 ACAATTGAATCTCGAGATACGGGCACATACGGAATTTCTGTCGGGAGCGTTATCAAAA 1206  
Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1207 CCACCTGTAGAGAAGCTTTTTCGGCTGTCTCTAAAA 1243

## RESULT 3

US-07-649-591B-2  
; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: hybridization probe  
LOCATION: 133 to 178  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: potential clip site  
LOCATION: 380 to 382  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 41 to 106  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-649-591B-2  
Alignment Scores:  
Pred. No.: 6.58e-213 Length: 1749  
Score: 1732.00 Matches: 338  
Percent Similarity: 86.01% Conservative: 0  
Best Local Similarity: 86.01% Mismatches: 0  
Query Match: 96.33% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCAAGTGGCCAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 40  
Db 167 CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGACCTTATT 226  
Qy 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAAATGTGAAGCC 286



Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
Db 287 CATTTAAATGTGACGGAATTCATGTCAGTGTCTGTGTCGACAGCGTGGAGATCTTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCCACGACACAGTCAGCCCCGAGCCTCCGATCGTACTATGAACAG 406  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTTATACTGAGAGCATCTCTGAT 466  
Qy 121 MetLeuThrIleHisIleGlySerPheGluIleTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTCAAAAATCCCATGTCCTCTCTGTCATTTGAGAAGTACCCACTCTATGTTTAAAG 526  
Qy 141 ValSerGlyIleGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTTCTGGAAAGAACAAACAGCCAAATGCCATATGGATTGACTGTGGATCCATGCC 586  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 587 AGAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAACTCAATTCAT 646  
Qy 175 ----- 175  
Db 647 GGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706  
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
Db 707 GTTAATGTGGCGTTATGACTACTCATGGAAGAAAGATCGAATGTGGAGAAAGACCGT 766  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 767 TCTTTCTATGCGAACAATCATGTCATCGAACACCTGAATAGCAACTTTGCTTCCAAA 826  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 827 CACTGGTGTGAGGAAGTGCATCCAGTTCCTCATCTCGGAACCTACTGTGGACTTTAT 886  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 887 CCTGAGTCAGAACCCAGAGTGAAGCAGTGGCTAGTTTCTTGAGAAGAAATATCAACAG 946  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 947 ATTAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTAT 1006  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 1007 ACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGT 1066  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1067 GCTATTGAGAAAATAGTAAATAACAGGTATACATAGCCCATGCTCAGAAACCTTA 1126  
Qy 304 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1127 TACCTAGTCTCTGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAATATTCGTTT 1186  
Qy 324 -----ThrSerAs 326  
Db 1187 ACAATTGACTTCGAGATACGGGCACATACGGATTTCTGTGCGCGGCGGTATACATAA 1246  
Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1247 CCCACCTGTAGAGAAGCTTTTGCCGCTGCTCTCTAAA 1283

## RESULT 4

US-08-277-540-2

; Sequence 2, Application US/08277540

; Patent No. 5474901

; GENERAL INFORMATION:

; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-277-540-2  
  
Alignment Scores:  
Pred. No.: 6.58e-213 Length: 1749  
Score: 1732.00 Matches: 338  
Percent Similarity: 86.01% Conservative: 0  
Best Local Similarity: 86.01% Mismatches: 0  
Query Match: 96.33% Indels: 55  
DB: 1 Gaps: 2  
  
US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)  
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuLeu 40  
Db 167 CAGATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226  
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAsnValLysAla 60  
Db 227 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTCATGTGCAATGTGAAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
Db 287 CATTTAAATGTGACGGAATTCATGCACTGTCTTGTGTCGACAGCTGGAGATCTTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCCACGACACAGTCAGCCCCGAGCCTCCGATCGTACTATGAACAG 406



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Qy 101 TyrHisSerLeuAenGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATCTTGGATAGATTTATTAACAGAGGACCTCTGAT 466
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAAATCCCAATGGATCTCATTTGAGAAGTACCACCTCTATGTTTAAAG 526
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTTCGTGAAAGAACCAACAGCCAAATGCCATATGGATTGACTGGGAATCCATGCC 586
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAATGGATCTCTCTGCTTCTGCTTGGTTTCATAGGCCATATAAATCAATTCAT 646
Qy 175 ----- 175
Db 647 GGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183
Db 707 GTTAATGTGGACGGTTATGACTACTATGGAAAAAGAAATCGAATGTGGAGAAACCGT 766
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 767 TCYTTCATATGGCAACATCATTTGATCGAACACACCTGATAGAACTTTGCTTCCAAA 826
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTAT 886
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACACAGAAAGTGAAGCGAGTGCTAGTTTCTTGAGAGAAATATCAACCAG 946
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATACATCAGATGCATTCATCTCCAGCATATAGTGTTCATATTCCTAT 1006
Qy 264 ThrArgSerLysSerLysAspHisGluGluSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACAGAAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCTGT 1066
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAACTAGTAAAAATACCAGGTATACATGGCCATGGCTCAGAAACCTTA 1126
Qy 304 TyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1127 TACTAGCTCTGGAGGTGGGACAGTTGGATCTATGATTTGGGCATCAAAATATTCGTTT 1186
Qy 324 -----ThrSerAs 326
Db 1187 ACATTGAACCTTCGATACGGGCACATACGGATTCTTGCTGCGGAGCGTTATACATA 1246
Qy 326 nProProValGluLysLeuProLeuSerLeuLys 338
Db 1247 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTATAAA 1283
RESULT 5
US-08-430-787A-2
; Sequence 2, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-430-787A-2
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Alignment Scores: 6.58e-213 Length: 1749
Pred. No.: 1732.00 Matches: 338
Score: 86.01% Conservative: 0
Percent Similarity: 86.01% Mismatches: 0
Best Local Similarity: 96.33% Indels: 55
Query Match: 1 Gaps: 2
DB:
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US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCCAGAACCTCTAGGCAAGTTCAAGTTCTA 166
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 167 CAGACTTCTACACATATGAGATTGTTCTCTGCGAGCGGTAAACAGCTGACCTTATT 226
Qy 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspValLeuAla 60
Db 227 GTGAAGAAAAACAAGTCCATTTTGTAAATGTCATCTGATGTCGACAAATGTGAAGCC 286
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTGAGCGGAATTCATGCTGCTGCTGCGACAGCTGGAAGATCTTATT 346
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTTCCAAACGACACAGTCAGCCCCCGAGCCTCCCGCATCTGTAACAG 406
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATTTCTGGATAGAAATTTATTAACAGAGGACCTCTGAT 466
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Qy	121	MetLeuThrIysIleHisIleGlySerSerPheGluIysTyrProLeuTyrValLeuLys	140
Db	467	ATGCTTACAAAAATCCCAATTGGATCCTCAATTTGAGAAAGTACCCACACTCTATGTTTAAAG	526
Qy	141	ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrrPileAepCysGlyIleHisAla	160
Db	527	GTTTCTGGAAAAGAACAAACAGCCAAATAATGCCATATGGATTGACTGTGGAAATCCATGCC	586
Qy	161	ArgGlnTrrPileSerProAlaPheCysLeuTrrPheIleGlyHis	175
Db	587	AGAGAAATGGATCTCTCTGCTTTCTGTGGTTCTATAGGCCATATAAAGCTCAATTCAT	646
Qy	175	-----	175
Db	647	GGGATAATAGGCCAATATACCAATCTCTCGAGGCTGTGGATTTCCTAATGTTATGCGGGT	706
Qy	176	-----AsnArgMetTrrPrrqLysAsnArg	183
Db	707	GTTAAATGTGACGGTTATGACTACTCATGGAAAAAGAAATCGAATGTGGAGAAAGAACCGT	766
Qy	184	SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys	203
Db	767	TCATTCTATCGAAACAATCATTTGCATCGGAACAGACCTGAATAGGAACATTGTCTTCCAAA	826
Qy	204	HisTrrPrrCysGluGluGlyAlaSerSerSerSerGlnThrTrrTyrCysGlyLeuTyr	223
Db	827	CACGTGGTGTGAGGAAGGTGATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTAT	886
Qy	224	ProGluSerGluProGluValLysAlaValaSerPheLeuArgArgAsnIleAsnGln	243
Db	887	CCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTTCTTTGAGAGAAATATCAACCAAG	946
Qy	244	IleLysAlaTrrIleSerMetHisSerTyrSerGlnHisIleValPheProTrrSerTyr	263
Db	947	ATTTAAAGCATACATCAGCATGCATTCATCTACTCCAGCATATAGTGTTCCTCATATTCCTAT	1006
Qy	264	ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg	283
Db	1007	ACAGAAAGTAAAGCAAAAGCAATGAGGAACCTGTCTCTAGTAGCCAGTGAAGCAATTCGT	1066
Qy	284	AlaIleGluLysThrSerLysAsnThrArgTrrThrHisGlyHisGlySerGluThrLeu	303
Db	1067	GCTATTGAGAAAACTAGTAAAAATACCAGGTATACATGCGCATGCTCAGAAAAACCTTA	1126
Qy	304	TyrLeuAlaProGlyGlyGlyAspAsnTrrIleTrrAspLeuGlyIleLysTrrSerPhe	323
Db	1127	TACCTAGTCTCTGGAGGTGGGACGATGGATCTATGATTGGGCATCAAAATATTCGTTT	1186
Qy	324	-----ThrSerAs	326
Db	1187	ACAATTGAACCTTCGAGATACGGGCACATACGGATTCTTCGTGCGGAGCGTTACATCAAA	1246
Qy	326	nProProValGluLysLeuLeuProLeuSerLeuLys	338
Db	1247	CCCAACCTGTAGAGAAGCTTTTTCGCGCTGCTCTCTAAAA	1283

## RESULT 6

US-08-696-139-1

03-08-030 133 I  
; Sequence 1, Application US/08696139

; Sequence 1, Application No. 5672496  
; Patent No. 5672496

; FACILE NO: 3672456  
; GENERAL INFORMATION:

APPLICANT: Faverman, Jeffrey T.

APPLICANT: Fayerman, Jeffrey I.  
APPLICANT: Greenen. David P.

APPLICANT: Greenen, David P.  
APPLICANT: Hershberger, Charles L.

APPLICANT: Hershberger, Charlene  
APPLICANT: Larson, Jeffrey L.

APPLICANT: Larson, Jeffrey I.  
APPLICANT: Sterner, Jane I.

; APPLICANT: Sterner, Jane I  
: APPLICANT: Zhang Hai Zhao

APPLICANT: Zhang, Haichao

; DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; TITLE OF INVENTION:

; TITLE OF INVENTION: PA  
: NUMBER OF SEQUENCES. 6; NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS:  
ADDRESS: Elt Hill, and Comm.

CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696,139  
FILING DATE:

Alignment Scores:

Alignment Scores:		
Pred. No.:	4.55e-73	Length:
Score:	646.50	Matches:
Percent Similarity:	54.5%	Conservative:
Best Local Similarity:	37.9%	Mismatches:
Query Match:	35.9%	Indels:
DB:	1	Gaps:
		6

US-09-980-887A-3 (1-338) x US-08-696-139-1 (1-1215)

Qy	1	PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu	20
Db	28	TTCGAAGGGGAGAAGGTGTTCCGTGTCATGTGTTGAAGATGAAATGACATCAGCTTACTC	87
Qy	21	GlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle	40
Db	88	CATGAGTTGGCCAGCACGAGCATGTCCTCTGGAACCCAGATTCTGTGTACACAAATC	147
Qy	41	VallYsLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVallYsAla	60
Db	148	AAACCTCACGTACAGTTGACTTCCGTGTGAAGCAGCAAGATATTTGGCTGTGGAGAC	207
Qy	61	HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle	80
Db	208	TTTCTGGAGCAGAATGAACACTACAAATATG/GGTACTCATAAACAACCTGAGATCTGTGCTC	267
Qy	81	GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln	100
Db	268	GAGGCTCATGTTTGACAGCAGAGTC-----CGTCAAACTGGACACAGTTATGAGAAG	318
Qy	101	TyrHisSerLeuAsnGluIleTyrSerPilleGluPheIleThrGluArgHisProAsp	120
Db	319	TACAACTGGGAAACCATCGAGGCTTGACTAAGCAAGTCACCAAGTGAATAATCCAGAC	378
Qy	121	MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys	140
Db	379	CTCATCTCTCCACAGCCATCGGAATCATATTTTAGGAAACAATATATACATCTCTCAAG	438

141 ValSerGlyLysGluGlnThrAlaLysAsnAlaLeuTrpLeuPheCysGlyLeuHisAla 160  
142 |||||  
143 439 GTT---GGCAACCTGGACCAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 495  
144 |||||  
145 161 ArgGluTrpLeuSerProAlaPheCysLeuTrpPheLeu 173  
146 |||||  
147 496 AGAAGATGGATTTTCCCATGCAATTTTGGCAGTGGTTTGTGAGAGAGGCTGTTCACCTAT 555  
148 |||||  
149 173 ----- 173  
150  
151 556 GGATATGAGATCATGACAGCAATTCCTCAACAGCTAGACTTTTATGTCTTGCCTGTG 615  
152 |||||  
153 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183  
154 |||||  
155 616 CTCAATATTGATGCTACATCTACACCTGGACCAAGAACCGAATGTGAGAGAGCCGC 675  
156 |||||  
157 184 SerPheTrpAlaAsnHisCysLeuGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
158 |||||  
159 676 TCTACCAATGCTGGAATCTGCTGATTTGGCAGACCCCAACAGAAATTTT---GATGCT 732  
160 |||||  
161 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTrpCysGlyLeuTrp 223  
162 |||||  
163 733 GGGTGGTGCAACTGGAGCTCTACAGACCCCTGGCATGAGACTTACTGTGATCTGCT 792  
164 |||||  
165 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnLeuAsnGln 243  
166 |||||  
167 793 GCAGAGTCTGAAAGAGACCAAGGCCCTGGCTGATTTTATACGCAACACCTCTCTCC 852  
168 |||||  
169 244 IleLysAlaTrpLeuSerMetHisSerTrpSerGlnHisLeuPheProTrpSerTrp 263  
170 |||||  
171 853 ATCAAGCATACCTGACGATCCATCTACTACTCAGATGATCTACTACCCCTTATCTCTAT 912  
172 |||||  
173 264 ThrArgSerLysSerLysAspHisGluGluSerLeuValAlaSerGluAlaValArg 283  
174 |||||  
175 913 GATTACAACTCCCGAGAACATGCTGAGTTGATTAACCTGGCTAAGCTGCGTGAA 972  
176 |||||  
177 284 AlaIleGluLysThrSerLysAsnThrArgTrpHisGlyHisGlySerGluThrLeu 303  
178 |||||  
179 973 GAAGTT---GCTACACTGTATGGCACCACCAAGTACATACACGCCGCCAGGAGCTACAACAATC 1029  
180 |||||  
181 304 TyrLeuAlaProGlyGlyLysAspAspTrpLeuTrpLeuGlyLysTrpSerPhe 323  
182 |||||  
183 1030 TATCCTGCTGCTGGGCTCTGATGCTGGGCTTATGACCAAGGAATCAAATATTCCTTC 1089  
184 |||||  
185 324 Thr 324  
186 |||||  
187 1090 ACC 1092

## RESULT 7

US-08-860-882A-56  
; Sequence 56, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGELE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-56

## Alignment Scores:

Pred. No.:	7,07e-72	Length:	1263
Score:	637.50	Matches:	130
Percent Similarity:	54.85%	Conservative:	68
Best Local Similarity:	36.01%	Mismatches:	120
Query Match:	35.46%	Indels:	43
DB:	2	Gaps:	6

US-09-980-881A-3 (1-338) x US-08-860-882A-56 (1-1263)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db |||||  
58 TTTGAGGCGAGAGAGGTGTTCCGTGTTAAGATGAAATACATTAACATAATC 117  
QY 21 GlnAsnLeuThrThrTrpGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db |||||  
118 CGGAGTTGGCAGACGACCCAGATTGACTTCTGGAAGCCAGATTCTGTACACAAATC 177  
QY 41 ValLysLysGlnValHisPheValAsnAlaSerAspValAsnValLysAla 60  
Db |||||  
178 AAACCTCAGTACAGTTCGCTGTTAAAGCAGAGAGATCTGCTACTGTGGAGAT 237  
QY 61 HisLeuAsnValSerGlyLeuProCysSerValLeuAlaAspValGluAspLeu 80  
Db |||||  
238 GTTAAAGCAGAGATGAACATAACAAGTACTGATAAGCAACCTGAGAAATGTGGT 297  
QY 81 GlnGlnLysSerAsnAspThrValSerProArgAlaSerAlaSerTrpTrpGluGln 100  
Db |||||  
298 GAGGCTCAGTTGATAGCCGGT-----CGTGCAACAGGACACAGTTATGAGAG 348  
QY 101 TyrHisSerLeuAsnGluLeuTrpPheLeuPheLeuThrGluArgHisProAsp 120  
Db |||||  
349 TACAACAAGTGGGAACGATAGAGGCTTGACTCAACAAGTCCGCACTGAGATCCAGCC 408  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTrpProLeuTrpValLeuLys 140  
Db |||||  
409 CTCATCTCGCAGTGTATTATCGGAACCAACATTTGAGGAGCGGCTATTACCTCTCCTGAAG 468  
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaLeuTrpIleAspCysGlyLysAla 160  
Db |||||  
469 GTT---GGCAAGCTGGACAAATAAGCTGCCATTTTCATGAGACTGTGTTTCCAGGCC 525  
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheLeu 173  
Db |||||  
526 AGAGAGTGGATTTCTCTGCTGATTTCTGCCAGTGGTTGTAAAGAGAGGCTGTTCGTACCTAT 585  
QY 173 ----- 173  
Db 586 GGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCTGCTGTG 645

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Qy 174 -----GlyHis-----AsnArgMetTrrArgLysAsnArg 183
Db 646 CTCATATGATGCTCATCATCATCGACGACGCGGATTTGGAGAAAGACTCGC 705
Qy 184 SerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 706 TCCACCATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCT 762
Qy 204 HisTrpCysGluGluGlyAlaSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 763 GGTGGTGTGAATGAGGCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 822
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 823 GCAGAGTCTGAAAGGAGACCAAGCGCTGATTTCAATCCGCAACAACTCTCTCTCC 882
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 883 ATCAGGCATATCTGCAATCCATCTGCTACTCTCCCAATGATGATCTACCTTACTCATAT 942
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 943 GCTTACAACTCGGTGAGAACATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1003 GAACTT---GCCTCACTGCACGCGACCAAGTACATATATGCGCGGAGCTACCAACATC 1059
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTrrIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1060 TATCTGCTGCTGGGCTCTGACGCTTATGACCAAGGAATCAGATATCTCTTC 1119
Qy 324 Thr 324
Db 1120 ACC 1122

RESULT 8
US-09-011-769A-38
; Sequence 38, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAXEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 MB disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
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; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-011-769A-38

Alignment Scores:
Pred. No.: 7,07e-72 Length: 1263
Score: 637.50 Matches: 130
Percent Similarity: 54.85% Conservative: 68
Best Local Similarity: 36.01% Mismatches: 120
Query Match: 35.46% Indels: 43
DB: 4 Gaps: 6
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US-09-980-881A-3 (1-338) x US-09-011-769A-38 (1-1263)

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Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 58 TTGAGGCGGAGAGGTGTTCCGTGTAAGTGAAGATGAAATACATTAATAATC 117
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 118 CGCGAGTTGGCCAGCAGCCAGATTTCTTCTGGAAGCCAGATTTCTGTGCACAAATC 177
Qy 41 ValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
Db 178 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAGATGACTGTCTGTGGAGAT 237
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspLeuIle 80
Db 238 GTTCTAAAGCAGAGTAACTACATCACTGATGATGATGATGATGATGATGATGATG 297
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGln 100
Db 298 GAGGCTCAGTTTGTATAGCCGGTT-----CGTGCAACAGGACACAGTATATGAG 348
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisProAsp 120
Db 349 TACAACAAGTGGGAAACGATGAGGCTTCACTCAACAAGTCCGCTGAGATCCAGCC 408
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 409 CTCATCTCTCGCAGTGTATCGGAACCACTTTGAGGCGCGCGCTATTACCTCTCTGA 468
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 469 GTT---GGCAAGCTGGACAAAATAAGCTGCGCATTTTCATGAGCTGTGTGTTCCAT 525
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 526 AGAGAGTGGGATTTCTCTCTGATTTCTGCTGATGTTTGTAAAGAGAGGCTGTCTGTAC 585
Qy 173 ----- 173
Db 586 GGACGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGCTCTGTGTG 645
Qy 174 -----GlyHis-----AsnArgMetTrrArgLysAsnArg 183
Db 646 CTCATATGATGCTCATCATCATCGACGACGCGGATTTGGAGAAAGACTCGC 705
Qy 184 SerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 706 TCCACCATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCT 762
Qy 204 HisTrpCysGluGluGlyAlaSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 763 GGTGGTGTGAATGAGGCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 822
```

Db 763 GGTGGTGTGAATGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 822  
Qy 224 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 823 GCAGAGTCTGAAAGGAAACCAAGCCCTGGCTGATTTCATCCGCAACAACTCTCTTCC 882  
Qy 244 IleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 883 ATCAAGGCATATCTGCAATCCACTCGTACTCTCCCAATGATGATCTACCTTACTCATAT 942  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 943 GCTTACAACTCGGTGAGAACATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1003 GAACCTT---GCCTCACTGCGGACCAAGTACATATGCGCGGAGCTACAAACATC 1059  
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1060 TATCTGCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1119  
Qy 324 Thr 324  
Db 1120 ACC 1122

RESULT 9  
US-08-860-882A-71  
; Sequence 71, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGLETE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-PIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1284 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-860-882A-71  
Alignment Scores:  
Pred. No.: 7,27e-72 Length: 1284  
Score: 637.50 Matches: 130  
Percent Similarity: 54.85% Conservative: 68  
Best Local Similarity: 36.01% Mismatches: 120  
Query Match: 35.46% Indels: 43  
DB: 2 Gaps: 6

US-09-980-881A-3 (1-338) x US-08-860-882A-71 (1-1284)  
Qy 1 PheGlnSerGlyGlnValLeuAlaIleLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 85 TTTGAAGCGGAGAGGTGTTCCGTTTAAAGATTGAAGTAAATACATTAACATAATC 144  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 145 CGCGAGTTGGCCAGCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTGCACACAATC 204  
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAlaAspValLysAla 60  
Db 205 AAACCTCACAGTACAGTTGACTTCCGTTTAAAGCAGAGATGACTGTCACTGTGGAGAT 264  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 265 GTTCTAAAGCAGAAATGAACTTACAATACAAGTACTGTAAGCAACCTGAGAAATGTGGTG 324  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 325 GAGGCTCAGTTTGATAGCCGGTT-----CGTGCAACAGGACACACAGTTTATGAGAAG 375  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 376 TACAACAAGTGGGAAACGATAGAGGCTTGAACTCAACAAGTCCGCCACTGAGAAATCCAGCC 435  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 436 CTCATCTCTCGCAGTGTATTGGAACACCATTTGAGGAGCGCGCTATTACCTCTCTGAAG 495  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 496 GTT---GGCAAGCTGCGACAAAATAAGCTGCCATTTTCATGACTGTGTTTCCATGCC 552  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173  
Db 553 AGAGAGTGGATTTCTCTGCAATTCCTCCAGTGGTTTGTAAAGAGAGCGCTGTTCGTACCTAT 612  
Qy 173 ----- 173  
Db 613 GGACGTGAGATCCAACTGACAGAGCTTCTCGACAAGTTAGACTTTTATGTCCTGCTGTG 672  
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183  
Db 673 CTCATATTATGATGGCTTACATCTACACTGGACCAAGAGCGGATTTTGGAGAAAGACTCGC 732  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 733 TCCACCCACTCTGGATCTAGCTGCAITGGCAGACACCCCAACAGAAATTTT---GATGCT 789  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 790 GGTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAAACTTACTGTGGACCTGCC 849  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 850 GCAGAGTCTGAAAAGGAGACCAAGGCCCTGGCTGATTTCATCGCAACAACTCTCTTCC 909  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 910 ATCAAGGCATATCTGCAATCCACTCGTACTCCCAATGATGATGATGATGATGATGATGAT 969  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283



Db 1030 GAACTT---GCTCACTGACGGACCAAGTACACATATGCCCCGGGAGCTACACAAATC 1086  
Qy 304 TyrLeuAlaProGlyGlyAspTrpIleTyrAspLeuGlyVileLysTyrSerPhe 323  
Db 1087 TATCTGCTGCTGGGGCTCTGACGACTGGCTTATGACCAAGGATCAGATATTCCTTC 1146  
Qy 324 Thr 324  
Db 1147 ACC 1149

## RESULT 11

US-09-023-655-1020  
; Sequence 1020, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023.655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1020:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1622 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g179933  
; US-09-023-655-1020

Alignment Scores:  
Pred. No.: 1.09e-69 Length: 1622  
Score: 622.00 Matches: 128  
Percent Similarity: 55.12% Conservative: 71  
Best Local Similarity: 35.46% Mismatches: 118  
Query Match: 34.59% Indels: 44  
DB: 4 Gaps: 7

US-09-980-881A-3 (1-338) x US-09-023-655-1020 (1-1622)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 61 TTTGACAGGGAGAGGTTGTTCCCGGTGAAGCCCGCAGGATGAAAAACAAGCAGACATCAT 120

Qy 21 GlnAsnLeuThrThrThrTyrGluValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 121 AAGGACTTGGCCAAACCAATGAGCTTGATCCAGGTGCCACCCACCGTA 180  
Qy 41 ValLysLysGlnValHisPheValAsnAlaSerValAspValAsnValLysAla 60  
Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaLeuValAspLeuIle 80  
Db 241 GCCTTGGATCAAAATAAATGCACTATGAATCTTGATTCATGATCTACAGAAGAGATT 300  
Qy 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99  
Db 301 GAGAAACAGTTTGATGTTTAAAGAAGATATCCAGGACGACACAGC-----TACGCA 351  
Qy 100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119  
Db 352 AAATACAAATAATTGGGAAAAGATTGTGGCTTGGACTGAAAAGATGATGATAGTATCCT 411  
Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139  
Db 412 GAAATGGTCTCTCGATTAAATTTGATCTACTGTGAAGATATCCACTATATGTTCTG 471  
Qy 140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159  
Db 472 AAGATT---GGGAAAAGATGAAAGAAGAGCTATTTTATGGATTGTGGCATTCAC 528  
Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173  
Db 529 GCACGAGATGGGTCTCCCGCAGCATTTCTGCGAGTGTGTTCTCTATCAGGCAACCAAAACT 588  
Qy 173 ----- 173  
Db 589 TATGGGAGAAAACAAATATTATGACCAAACTCTTGGACCGAATGAATTTTATCTTCCT 648  
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182  
Db 649 GTGTTCAATGTTGATGATATATTTGGTCATGACAAAGAACCGCATGTGGAGAAAAT 708  
Qy 183 ArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202  
Db 709 CGTTCCAAGAAACCAAACTCCAAATGCATCGGCACTGACCTCAACAGGAATTTT---AAT 765  
Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeu 222  
Db 766 GCTTCATGGAACTCCATTCTTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825  
Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242  
Db 826 GCACCAAGATCCGAGAAAGAGACGAAGCTGTCTCACTAATTTTATTAGAAGCCACCTGAAT 885  
Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262  
Db 886 GAAATCAAGGTTTATACATCACTTCCATTCTCTACTCCAGATGCTATTGTTTCCCTATGGA 945  
Qy 263 TyrThrArgSerLysSerLysAspHisGluLysSerLeuValAlaSerGluAlaVal 282  
Db 946 TATACATCAAAACTGCCACCTACCATGAGGACTTGGCCAAAGTTGCAAGATTGGCACT 1005  
Qy 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302  
Db 1006 GATGTTCTA---TCAACTGATATGAACCCGCTACATCTATGGCCCAATAGATCAACA 1062  
Qy 303 LeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleTyrSer 322  
Db 1063 ATTTACCGGATATCAGGTTCTTCTTTAGACTGGGCTTATGACCTGGGCATCAACACACA 1122

Qy 323 Phe 323

Db 1123 TTT 1125

RESULT 12









Db 355 TACAACAGTGGGAAACGATAGAGCGTTGGACTCAACAAAGTCGCCACTGAGATCCAGCC 414  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 415 CTCATCTCTCGACGTGTTATCGGAACACACATTTGAGGAGCGCGCTATTACCTCCTGAAG 474  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 475 GTT---GGCAAGCTGGCAAAATAGCGCTGCCATTTTCAGGAGCTGGGTTTCCATGCC 531  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173  
Db 532 AGAGAGTGGATTTCTCTGCAATTTCTGCCAGTGGTTTGTAGAGAGGCTGTTGCTACCTAT 591  
Qy 173 ----- 173  
Db 592 GGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAAAGTTAGACTTTTATGTCCTCGCTGTG 651  
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183  
Db 652 CTCATATATGATGCTACATCTACACCTGGACCAAGACCGATTTTGGAGAAAGACTCGC 711  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 712 TCCACCCATCTGATCTAGCTGCTGATGGACACACACCCCAACAGAAATTTT---GATGCT 768  
Qy 204 HisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 769 GGTGGTGTGAATTTGGAGCCCTCTCGAAACCCCTGTGTATGAACCTTACTGTGGACCTGCC 828  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 829 GCAGAGTCTGAAAGGAGCAACAGGCCCTGCTGATTTTCATCCGCAACAACTCTCTCC 888  
Qy 244 IleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 889 ATCAAGGATATCTGCACATCTACCTGCTACTCCCAATGATGATCCTACCTTACTCATAT 948  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 949 GCTTACAAACTCGGTGAGAACAACTGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1008  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1009 GAACCTT---GCCTCAGTCACGCGCACCAAGTACACATATGCGCGGAGCTACAAACATC 1065  
Qy 304 TyrLeuAlaProGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1066 TATCTTCTGCTGGGACTTCTAAAGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1125  
Qy 324 Thr 324  
Db 1126 ACC 1128

## RESULT 15

US-08-782-760-5  
; Sequence 5, Application US/08782760  
; Patent No. 5948668  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Jacob  
; APPLICANT: Fulga, Netta  
; APPLICANT: Mendelovitch, Simona  
; APPLICANT: Gorecki, Marian  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; NUMBER OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/782,760  
FILING DATE: 13-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/378,233  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0336/43847  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 927 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..927  
US-08-782-760-5

## Alignment Scores:

Pred. No.:	1,47e-68	Length:	927
Score:	610.00	Matches:	126
Percent Similarity:	60.50%	Conservative:	44
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Query Match:	33.93%	Indels:	41
DB:	2	Gaps:	5

US-09-980-881A-3 (1-338) x US-08-782-760-5 (1-927)

Qy	93	AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu	112
Db	1	GCAAGTGGACACAGCTACACCAAGTACACAACTGGGAAACGATTGAGGGGTGATTCAA	60
Qy	113	PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu	132
Db	61	CAAGTTGCCACTGATAATCCAGACCTTGACCTCAGAGCGCTCATTTGGACACACATTGAA	120
Qy	133	LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle	152
Db	121	GGACGTAACATGATGTCTCTCAAGATT---GGTAAACTAGACCGGAATAAGCCTGCCATC	177
Qy	153	TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe	172
Db	178	TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTCTCTCGCATTTCTGTCAGTGGTTT	237
Qy	173	Ile-----	173
Db	238	GTGAGAGGCTGTCCGTACCTATATATCAGAGATCCACATGAACAGCTTCTAGATGAA	297
Qy	174	-----GlyHis-----	175
Db	298	CTGGATTCTATGTTCTGCTGCTGCTGCTCAACATTGATGGCTATGTCTACCTGAGCTAAG	357
Qy	176	AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp	195
Db	358	GACAGAAATGTGGAGAAAAACCCGCTCTACTATGCTGGTGAAGTTCCTCTGCTGGGTGAC	417
Qy	196	LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys	215

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Db 418 CCCAACAGGAATTTT--AATGCTGGCTGGTGTGAAGTGGAGGCTTCTCGAGTCCCTGC 474
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235
Db 475 TCTGAACCTTACTGTGGACCCAGCCAGAGTCTGAAAAAGAGACAAAGGCCCTGGCAGAT 534
Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255
Db 535 TTCATCGCAACAACCTCTCCACCATCAAGGCCCTACCTGACCATCCACTCATACTCAG 594
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 275
Db 595 ATGATGCTCTACCCCTTACTCTATGACTACAAACTGCTGAGAACTATGAGGAATTGAAT 654
Qy 276 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295
Db 655 GCCCTGGTGAAGGTGGGCAAGGAGCTT---GCCACTCTGCATGGCACCACCAAGTACACA 711
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyr 315
Db 712 TATGGCCCGAGGACTACAAACAATCTATCTGCTGCTGGGGATCTGACGACTGGTCTTAT 771
Qy 316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 335
Db 772 GATCAGGAATCAAAATATTCCTTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830
Qy 336 Ser 336
Db 831 TCT 833
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Job time : 110.464 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 588.636 Seconds  
(without alignments)  
2944.316 Million cell updates/sec

Title: US-09-980-881a-3

Perfect score: 1798

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Searched: 3413475 seqs, 256380928 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0  
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Database : Published Applications NA:\*

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- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	1749.5	97.3	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1749.5	97.3	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1732	96.3	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1708.5	95.0	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1708.5	95.0	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1628	90.5	1272	15	US-10-379-836-1	Sequence 1, Appli
7	1329.5	73.9	1037	16	US-10-115-479-63	Sequence 63, Appl
8	1290.5	71.8	1132	16	US-10-115-479-65	Sequence 65, Appl
9	902	50.2	1400	9	US-09-925-302-24	Sequence 24, Appl
10	902	50.2	1400	10	US-09-925-302-24	Sequence 24, Appl
11	622	34.6	1254	14	US-10-229-546-3	Sequence 3, Appli
12	622	34.6	1622	14	US-10-229-546-1	Sequence 1, Appli
13	622	34.6	1622	15	US-10-429-802-21	Sequence 21, Appl
14	622	34.6	1622	16	US-10-430-503-12	Sequence 12, Appl
15	622	34.6	1622	16	US-10-262-511-71	Sequence 71, Appl
16	622	34.6	1622	16	US-10-641-643-1020	Sequence 1020, Ap
17	622	34.6	1633	15	US-10-341-434-187	Sequence 187, App
18	622	34.6	1740	14	US-10-116-802-95	Sequence 95, Appli
19	619.5	34.5	1302	17	US-10-477-515-1	Sequence 1, Appli
20	619.5	34.5	1311	13	US-10-200-344-9	Sequence 9, Appli
21	619.5	34.5	1993	15	US-10-274-639-33	Sequence 33, Appl
22	619.5	34.5	1993	16	US-10-333-574-33	Sequence 33, Appl
23	619.5	34.5	2154	9	US-09-910-059-124	Sequence 124, App
24	618	34.4	1332	9	US-09-954-456-1141	Sequence 1141, Ap
25	617.5	34.3	1907	18	US-10-757-262-127	Sequence 127, App
26	591	32.9	416	9	US-09-960-352-14595	Sequence 14595, A
27	571.5	31.8	2128	13	US-10-200-344-13	Sequence 13, Appl
28	569	31.6	1125	9	US-09-888-615-2	Sequence 2, Appli
29	569	31.6	1332	15	US-10-176-306-75	Sequence 75, Appl
30	569	31.6	1603	15	US-10-176-306-73	Sequence 73, Appl
31	562	31.3	1826	15	US-10-252-157-453	Sequence 453, App
32	554	30.8	1200	14	US-10-200-910-7	Sequence 7, Appli
33	554	30.8	1200	18	US-10-843-130-7	Sequence 7, Appli
34	549	30.5	1870	9	US-09-910-059-112	Sequence 112, App
35	549	30.5	1870	17	US-10-608-710-3	Sequence 3, Appli
36	534.5	29.7	1050	13	US-10-200-344-11	Sequence 11, Appl
37	533.5	29.7	991	16	US-10-383-201-93	Sequence 93, Appl
38	527.5	29.3	1260	16	US-10-257-174-16	Sequence 16, Appl
39	527.5	29.3	1311	14	US-10-200-910-5	Sequence 5, Appli
40	527.5	29.3	1311	16	US-10-257-174-15	Sequence 15, Appl
41	527.5	29.3	1311	17	US-10-451-821-1	Sequence 1, Appli
42	527.5	29.3	1311	18	US-10-843-130-5	Sequence 5, Appli
43	527.5	29.3	1348	16	US-10-072-012-315	Sequence 315, App
44	527.5	29.3	1641	17	US-10-381-820A-5	Sequence 5, Appli
45	523.5	29.1	1295	17	US-10-363-829-148	Sequence 148, App

ALIGNMENTS

RESULT 1

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:

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Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservatives: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCCAAGTTCTAGCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTCTTACTCAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 202

Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAACCAAGTCCATTTTGTAAATGCACTGATGTCGACAAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATTCATGCACTCTTCTGGCAGCTGTTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCACGACACAGTACAGCCCGGAGCCCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluAtrGHisProAsp 120  
Db 393 TATCACTCACATAATGAATCTTCTTGGATAGAAATTTAATCTGAGGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAATCCACATTTGATGCTCTTCTAGAAAGTACCCACTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGAAAAGAACCAAGACGACCAAAATGCCATATGATGATGCTGTGGAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 563 AGAGAAATGGATCTCTCTGCTCTTCTGCTTGGTTTCATAGGCCAATATCGAATGTGAGA 622

Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGTTCTTCTATGCGAACAATCATTTGCAATCGGAACAGACCTGAAATAGGAACCTTT 682

Qy 201 AlaSerLysHisTrpCysGluGluClyAlaSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGTGTGAGAAAGGTGCATCCAGTTCTCTCATGCTCGGAAACCTACTGT 742

Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 240  
Db 743 GGACTTTATCTGAGTCAAGACCAAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAAGAAAT 802

Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACACAGATTAAAGCATACATCAGCATGATCCATCTACTCCAGCATATAGTGTTCCTCA 862

Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCCTATACACGAAAGTAAAGCAACACCATGAGGAAGTGTCTCTAGTAGCCAGTGAA 922

Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCGTGCTATTGAGAAATAGTAAATAATACAGGTATACATATGGCCATGGCTCA 982

Qy 301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 320  
Db 983 GAAACCTTTATACCTCTCTGGAGTGGGAGCGAGTATGATCTATGATTTGGGCATCAAA 1042

Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCGTTTCAATGAACTTCGAGATACGGGCACATACGAGATCTTCTGTCGGGACGCT 1102

Qy 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTTAAAA 1148

RESULT 2  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

Alignment Scores:  
Pred. No.: 6,31e-206 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservatives: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 14 Gaps: 1

US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTCCAGAGTGCCCAAGTTCTAGCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTCTTACTCAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 202

Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAACCAAGTCCATTTTGTAAATGCACTGATGTCGACAAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATTCATGCACTCTTCTGGCAGCTGTTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCACGACACAGTACAGCCCGGAGCCCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluAtrGHisProAsp 120  
Db 383 TATCACTCACATAATGAATCTTCTTGGATAGAAATTTAATCTGAGGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAATCCACATTTGATGCTCTTCTAGAAAGTACCCACTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGAAAAGAACCAAGACGACCAAAATGCCATATGATGATGCTGTGGAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180

Db 563 AGAGAAATGGATCTCTCTGCTTCTCTGCTTGTGGTTTCATAGGCCATAATCGAATGTGGAGA 622  
Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGCTTCTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAAATAGGAATCTT 682  
Qy 201 AlaSerLysHisTyrCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTATGCTCGAAACCTACTGT 742  
Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 240  
Db 743 GGACTTTATCTCGTGCAGAACACAGAGTGAAGCAGTGGCTAGTCTTCTTGAGGAAGAAAT 802  
Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACCAAGATTAAGGCATACATCAGCATGCATTCATCTACCTCCAGCATATAGTGTTC 862  
Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCTATACACGAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCCAGTGAA 922  
Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCTGTGCTATTGAGAAATAGTAAATAATACCAAGGTATACACATGGCCATGGCTCA 982  
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 320  
Db 983 GAAACCTTTATACCTAGCTCTCGAGGTGGGACGATTTGGATCTATGATTTGGGCATCAA 1042  
Qy 321 TyrSerPhe----- 323  
Db 1043 TATTGGTTTCAATGAATTCGAGATACGGGCACATACGGAATCTTGTGCGCGAGCGT 1102  
Qy 324 -ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAACCCACCTGTGAGGAAGCTTTTCCGCTGTCTCTAATA 1148

## RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Uwe  
; APPLICANT: Scherf, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

## Alignment Scores:

Pred. No.:	1,03e-203	Length:	1728
Score:	1732.00	Matches:	338
Percent Similarity:	86.01%	Conservative:	0
Best Local Similarity:	86.01%	Mismatches:	0
Query Match:	96.33%	Indels:	55
DB:	9	Gaps:	2

US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)  
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTTCAGAGTGGCCAAAGTTCTAGCTGTCTTTCTTAGAACCTCTTAGGCAAGTTCAAGTTCTA 145  
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 40  
Db 146 CAGATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAAACAGCTGACCTTATT 205  
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 206 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTCATGTGCGAATGTGAAAGCC 265  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 266 CATTTAAATGTAGCGGAATTCATGCGGTCTTGTGCGACGCTGGGAAGATCTTATT 325  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 326 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGACAG 385  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATACTGAGAGCATCTCGAT 445  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 446 ATGCTTACAAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCACCTCTATGTTTAAAG 505  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 506 GTTTCTGGAAGAAAGACAAACAGCCAAAATGCCATATGGATTGACTGTGGAAATCCATGCC 565  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175  
Db 566 AGAGAATGGATCTCTCTGCTTCTCTGCTTCTGCTTCTATAGGCCATATAAATCAATCTAT 625  
Qy 175 ----- 175  
Db 626 GGGATAATAGGGCAATATACCAATCTCTGAGCGTTGTGGATTTCTATGTTATGCCCGGTG 685  
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
Db 686 GTTAATGTGACGGTTATGACTACTCATGGAAGAAAGATCCAAATGTGGAAGAAACCGT 745  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 746 TCTTTCTATGCGAACAATCATTCATCGGAACAGACCTGAATAGGAACCTTTGCTTCCAAA 805  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 806 CACTGGTGTGAGGAAGTGCATCCAGTTCTCATGCTCGGAAACCTACTCTGGACCTTAT 865  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 866 CCTGAGTCAGAACCAAGTGAAGGAGGCTGGCTAGTTCTTGAGAGAAATATCAACAG 925  
Qy 244 IleLeuAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 926 ATTAAGCATACATCAGCATGCTTCTATCTCCAGCATATAGTGTTCATATTCCTAT 985  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 986 ACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAAGCATGTCGT 1045  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1046 GCTATTGAGAAAACTAGTAAAAATACCAAGGTATACATGCGCCATGGCTCAGAAACCTTA 1105  
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323

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Db 1106 TACCTAGCTCTGGAGGTGGGACGATGGATCTATGATTTGGGCATCAATATTCGTTT 1165
Qy 324 -----ThrSerAs 326
Db 1166 ACAATTGAATTCGAGATACGGCACATACGGAATTCCTGCTCGCGGAGCGTTACATCAAA 1225
Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1226 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1262

RESULT 4
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel W.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 FT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69
Alignment Scores:
Pred. No.: 5,59e-201 Length: 1344
Score: 1708.50 Matches: 336
Percent Similarity: 84.42% Conservatives: 0
Best Local Similarity: 84.42% Mismatches: 2
Query Match: 95.02% Indels: 60
DB: 16 Gaps: 3

US-09-980-881A-3 (1-338) x US-10-115-479-69 (1-1344)
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 97 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 156
Qy 21 GlnAsnLeuThrThrThrTyTGluLeuValLeuProValThrAlaAspLeuLeu 40
Db 157 CAGAAUCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 216
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 217 GTGAGAGAAAAACAGTCCATTTTGTGTAATGCATCTGATGTCGACATGTGAAGCC 276
Qy 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80
Db 277 CATTTAAATGTGAGCGGAATTCATGCAATGCTCTTGTCTGGCAGACGCTGGAAGATCTTATT 336
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 337 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCGCGCTCCGCATCGTACTATGAACAG 396
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTyrPheIleGluPheIleThrGluArgHisProAsp 120
Db 397 TATCACTCACTAAATGAATCTATTCTTGTAGATAATTTATACTGAGAGGCATCTCTGAT 456
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 457 ATGCTTACAAAAATCCACATTTGGATCTCTATTGAGAAGTACCACACTCTATGTTTAAAG 516
Qy 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAsp 155
Db 517 GGTTCCTTTGAGCAGGTTTCTGGAAAAAGAACAGACGCCAAATAATGCCATATGGATTGAC 576
Qy 156 CysGlyIleHisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 175
Db 577 TGTGGAATCCATGCCAGAGAAATGGATCTCTCCTGCTTTCTGCTGTGTTTCATAGGCCAT 636
Qy 175 ----- 175
Db 637 ATAACCTCAATTCATGGGATAATAGGGCUATATACCAATCTCCTGAGGCTTGTGGATTTC 696
Qy 176 -----AsnArgMet 178
Db 697 TATGTTATGCCGGTGGTTAATGTGGATGATGATGATGATGATGATGATGATGATGATG 756
Qy 179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198
Db 757 TGGAGAAAGAACCGTTCTTCTATGCGAACATCATTTGCATCGGAACAGACCTGAATAGG 816
Qy 199 AsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerSerSerSerSerSer 218
Db 817 AACTTTGCTTCCAAACACTGGTGTGAGAGAGGTGCATCCAGTTCCTCATGCTCGGAACCC 876
Qy 219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238
Db 877 TACTGTGACTTTTATCTGAGTCAGAACACAGAGAGTGAAGCAGTGGGTAGTTCTTTGAGA 936
Qy 239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258
Db 937 AGAAATATCAACACAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTG 996
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Qy	199	AsnPheAlaSerLysHisTrpCysGluGluClyAlaSerSerSerSerCysSerGluThr	218
Db	806	AACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGTCGGAAC	865
Qy	219	TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg	238
Db	866	TACTGTGGACTTTATCTCTGTAGTCCAGAACCCAGAGTGAAGGCGTGGCTAGTTCTTGAGA	925
Qy	239	ArgAsnIleAsnGlnIleLysAlaTyrIleSerMethHisSerTyrSerGlnHisIleVal	258
Db	926	AGAAATATCAACCAGATTTAAAGCATACATCAGCATGCATTCTACTCTCCAGCATATAGTG	985
Qy	259	PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla	278
Db	986	TTTCCATATCTCTATACCAAGATTAAGCAAGAACCATGAGGAACATGTCTCTAGTAGGCC	1045
Qy	279	SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis	298
Db	1046	AGTGAACGAGTTCGTGCTATTGAGAAATTAGTAAATAATACCAGGTATACACATGGCCAT	1105
Qy	299	GlySerGluThrLeuTyrLeuAlaProGlyClyAspAspTrpIleTyrAspLeuGly	318
Db	1106	GGCTCAGAAACCTTATACCTAGTCTCTGGAGTGGGACGATTGGATCTATGATTTTGGGC	1165
Qy	319	IleLysTyrSerPhe-----	323
Db	1166	ATCAATATTTCGTTTACAAATTGAACCTTCGAGATACGGGCACATACGAGTTCCTGCTGCCG	1225
Qy	324	-----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys	338
Db	1226	GAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTCGCCGTCTCTCTAAAA	1277

## RESULT 6

```

US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
; US-10-379-836-1

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Alignment Scores:	4.86e-191	Length:	1272
Pred. No.:	Score:	Matches:	318
	1628.00	Conservative:	9
Percent Similarity:	83.21%	Mismatches:	11
Best Local Similarity:	80.92%	Indels:	55
Query Match:	90.55%	Gaps:	2
DB:	15		

US-09-980-881A-3 (1-338) X US-10-379-836-1 (1-1272)

Qy	1	PheGlnSerGlyGlnValLeuAlaIalaLeuProArgThrSerArgGlnValGlnValLeu	20
Db	67	TTTCAGAGTGGCCAGGTTCTTCTAGCTGCTCTCTCTAGAACCTCTAGGC	126
Qy	21	GlnAsnLeuThrThrTyrgluileValLeuTpgGlnProValThrAlaAspLeuile	40
Db	127	CAGAACTCTTACTACAAATATGAGATCTCTCTGGCAGCGGTAAACAGCGG	186

## RESULT 7

US-10-115-479-63  
; Sequence 63, Application US/10115479  
; Publication No. US2004006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 63  
; LENGTH: 1037  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (41)..(1007)  
US-10-115-479-63

Alignment Scores:  
Pred. No.: 3 48e-154 Length: 1037  
Score: 1329.50 Matches: 272  
Percent Similarity: 76.40% Conservative: 0  
Best Local Similarity: 76.40% Mismatches: 2  
Query Match: 73.94% Indels: 82

DB: 16 Gaps: 2  
US-09-980-881A-3 (1-338) x US-10-115-479-63 (1-1037)  
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTTCTCCTAGAACCTCTAGGCAAGTTCAGTCTTA 166  
QY 21 GlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 167 CAGAACTTCTACTACAACATATGAGATGTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226  
QY 41 ValIleLysGlnValHisPheValAsnAlaSerValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGCATCTGATGTCGACAAATGTGAAGCC 286  
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 287 CATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGGCAGACGTGGAAGATCTTATT 346  
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrrGluGln 100  
Db 347 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 406  
QY 101 TyrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTTATAACTGAGAGGCATCTGAT 466  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrValLeuLys 140  
Db 467 ATGCTTACAAAAATCCACATCGGATCCTCATTTGAGAAGTACCACCTCTATGTTTTAAAG 526  
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTTCGAAAAAGAACACAGCAGCCAAAAATGCCATATGGATTGCAC----- 571  
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 571 ----- 571  
QY 181 LysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 571 ----- 571  
QY 201 AlaSerLysHisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrrCys 220  
Db 572 -----TGT 574  
QY 221 GlyLeuTyrrProGluSerGluProGluValLysAlaValAspSerPheLeuArgAsn 240  
Db 575 GGACTTTATCTCTGAGTCAGAACCAAGGTGAAGCAGTGGCTAGTTCTTTCGAGAAGAAAT 634  
QY 241 IleAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPhePro 260  
Db 635 ATCAACACAGATTAAGCATACATCAGCATGCTTTCATCTCCGACGATATAGTGTGTCCA 694  
QY 261 TyrrSerTyrrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 695 TATTCCTATACAGAAAGTAAAGAACCAAGCCTAGGAACTGTCTCTAGTACGAGTGAA 754  
QY 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrrThrHisGlyHisGlySer 300  
Db 755 GCAGTTCGTGCTATTGAGAAAATTAGTAAATAATACCAGGTATACATATGGCCATGGCTCA 814  
QY 301 GluThrLeuTyrrIleuAlaProGlyGlyAspAspTrpIleTyrrAspLeuGlyIleLys 320  
Db 815 GAAACCTTATACCTAGCTCTCTGGGAGTGGGACGATTGGATCTATGATTTGGGCATCAAA 874  
QY 321 TyrSerPhe----- 323  
Db 875 TATTCGTTTCAACTGAATTCAGATACCGGCACATACGGAATTCCTGTCGCCGAGCGT 934  
QY 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338

Db 935 TACATCAACCCACCTGTAGAGAGCTTTGGCCGCTGTCTCTATAAA 980  
|||||

RESULT 8

US-10-115-479-65  
; Sequence 65, Application US/10115479  
; Publication No: US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytsek, Kimberly A.  
; APPLICANT: Zernhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 65  
; LENGTH: 1132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (41)..(1103)  
US-10-115-479-65  
Alignment Scores: 2.74e-149 Length: 1132  
Pred. No.: 1290.50 Matches: 263  
Score:

Percent Similarity: 66.08% Conservative: 0  
Best Local Similarity: 66.08% Mismatches: 1  
Query Match: 71.77% Indels: 134  
Db: 16 Gaps: 4  
US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)  
Qy 1 PheGlnSerGlyGlnValValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCAAGAGTGGCCAAAGTTCTAGCTGCTCTTCCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTriDlnProValThrAlaAspLeuIle 40  
Db 167 CAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226  
Qy 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCATCTGTATGCGAATGTGAAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 287 CATTTAAATGTAGCGGAATTCATGCATGTCTTCTGGCAGACGTGGAGATCTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCACACGACACAGTCAAGCCCGAGCCTCCGCATCGTACTATGAACAG 406  
Qy 101 TyrHisSerLeuAsnGlnIleTyrSerTyrPheGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCAATAATGAAATCTATTCTTGTAGAAATTTATACTAGAGGCGATCTCGAT 466  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAAATCCACATGGATCTCTATTTGAGAAAGTACCACCTCTATGTTTTAAAG 526  
Qy 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAsp 155  
Db 527 GGTTTCTTTGAGCAGAGGTTTCTGGAAAGAAACAAAGCAGCCAAAAATGCCATATGGATTGAC 586  
Qy 156 CysGlyIleHisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 175  
Db 587 TGTGGAATCCATGCCAGAAATGGATCTCTCTCTGCTTTCTGCTTGTGTTGTCATAGGCCAT 646  
Qy 175 ----- 175  
Db 647 ATAACCTCAATTCTATGGGATAATAGGCGCIATATACCAATCTCCTGAGGCTTGTGATTTC 706  
Qy 176 -----AsnArgMet 178  
Db 707 TATGTTATGCGGTGGTTAATGTGGATGTTTATGACTACTCATGGAATAAATCGAATG 766  
Qy 179 TrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArg 198  
Db 767 TGGAGAAAGAACCCGTTCTTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAAATAGG 826  
Qy 199 AsnPheAlaSerLysHisTyrCysGluCugIlyValaSerSerSerSerCysSerGluThr 218  
Db 827 AACTTTCCTTCCAAACACTGCTGTGAGAGAGTGCATCCAGTTCTCTATGCTCGGAAACC 886  
Qy 219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238  
Db 887 TACTGTGGACTTTTATCCTGAG----- 907  
Qy 239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258  
Db 907 ----- 907  
Qy 259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValala 278  
Db 907 ----- 907  
Qy 279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298

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Db 907 ----- 907
Qy 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 318
Db 908 ---TCAGAACTTATACCTAGCTCTCGAGGTGGGACGATTGATGATTTGGGC 964
Qy 319 IleLysTyrSerPhe----- 323
Db 965 ATCAATATTTCGTTTACAATTGAACCTTCGAGATACGGGCACATACGGATTCTTCTGCTCCG 1024
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1025 GAGCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGCTGTCTCTAAAA 1076

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5.54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservative: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 9 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGAATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCATGGGATAATAGGSCAATATACCAATCTCTGAGGCTTGTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCGGTGGTTAATGTGGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
Qy 179 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTTCCTTCTATGCGAACAATCATTTGTCGGAACAGACCTGGAATAGGAA 249
Qy 199 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 219
Db 250 CTTTGCTTCCAAACACTGGTGTGAGGAGGTGGATCCAGTTCTCTCATGCTCGGAACCTTA 309
Qy 219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTTCTTGAGAG 369
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Qy 239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValph 259
Db 370 AAATATCAACCAAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGT 429
Qy 259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
Db 430 TCCATATTCTATACACGAAGTAAAGCAAAAGACCATTAGGAACTGTCTCTAGTAGCCAG 489
Qy 279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisG1 299
Db 490 TGAAGCAGATTTCGTCTATTGAGAAACTAGTAAANAATACCAAGGTATATACATGGCCATGG 549
Qy 299 YSerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyI1 319
Db 550 CTCAGAAACCTTATACCTAGCTCTCGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609
Qy 319 eLysTyrSerPhe----- 323
Db 610 CAAATATTTCGTTTACAATTGAACCTTCGAGATACGGGCACATACGGATTCTTGTGCGCGA 669
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 670 GCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGCTGTCTCTAAAA 719

RESULT 10
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5.54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservative: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 10 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGAATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCATGGGATAATAGGSCAATATACCAATCTCTGAGGCTTGTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCGGTGGTTAATGTGGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
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Qy 179 pAtGLyAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTTCCTTCATGCGAAACATCATTCATCGAAGACACCTGATAGGAA 249
Qy 199 nPheAlaSerIlyHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 219
Db 250 CTTTGTCTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTA 309
Qy 219 rCysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTTATCCTCGAGTCAGAACCAAGAGTGAAGGCAGTGGCTAGTTTCTTGGAAG 369
Qy 239 gAsnIleAsnGlnIleLysAlaTyrlleSerMetHisSerTySerGlnHisIleValPh 259
Db 370 AAATATCAACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTT 429
Qy 259 eProTySerTyThrArgSerIlySerLysAspHisGluGluLeuSerLeuValAlaSe 279
Db 430 TCCATATCTCATACAGAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAG 489
Qy 279 rGluAlaValArgAlaIleGluLysThySerLysAsnThrArgTyThrHisGlyHisG1 299
Db 490 TGAAGCAGTTCGTCTATTGAGAAACCTAGTAAATAATACCAGGTATACACATGGCCATGG 549
Qy 299 ySerGluThrLeuTyLeuAlaProGlyGlyGlyAspTrpIleTyTrAspLeuGlyI1 319
Db 550 CTCAGAACCTTATACCTAGTCTCTCGAGGTGGGAGCATTTGGAICTATGATTTGGGCAT 609
Qy 319 eLysTySerPhe----- 323
Db 610 CAATATTCGTTTACATTTGAACCTTCGAGATACGGGCACATACGGATTCTTGTGTCGGGA 669
Qy 324 -----ThrSerAsnProValGlnLysLeuLeuProLeuSerLeuLys 338
Db 670 GCGTTATCATCAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 719
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## RESULT 11

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US-10-229-546-3
; Sequence 3, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
; APPLICANT: Weich, Nadine S.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
; FILE REFERENCE: MP101-156P1RNM
; CURRENT APPLICATION NUMBER: US/10/229,546
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/316,575
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1254)
US-10-229-546-3
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Alignment Scores:
Pred. No.: 2,35e-66 Length: 1254
Score: 622.00 Matches: 128
Percent Similarity: 55.12% Conservative: 71
Best Local Similarity: 35.46% Mismatches: 118
Query Match: 34.59% Indels: 44
DB: 14 Gaps: 7
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US-09-980-881A-3 (1-338) x US-10-229-546-3 (1-1254)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

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Db 61 TTTGACAGGAGAGAGGTGTTCCGCGTGAAGCCCGAGGATCAAAAAACAAGCAGACATCAT 120
Qy 21 GlnAsnLeuThrThrThrTyrgluIleValLeuTyrGlnProValThrAlaAspLeuIle 40
Db 121 AAGGACTTGGCCAAAAACCAATGAGCTTGACTTCCTGGTATCCAGTGCCACCCACCAAGTA 180
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerValAspValAsnValLysAla 60
Db 181 GCTGCTAATATGATGTTGGATTTCAGAGTAGTGAGAGGAATCCCAAGCCATCCAGTCT 240
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 241 GCCTTGGATCAAAATAAATGACATGTAATCTGATTCTATCATGATCTACAAGAAGATTT 300
Qy 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyTrpGlu 99
Db 301 GAGAAACAGTTTGTATTAAGAAAGATATCCAGCAGGCACAGC-----TAGGCA 351
Qy 100 GlnTyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArgHisPro 119
Db 352 AAATACATTAATTTGGGAAAGATTTGGCTTGGACTGAAAGATGATGGATAGATATCTCT 411
Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyTrpProLeuTyValLeu 139
Db 412 GAAATGCTCTCGTATTAAATTTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471
Qy 140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
Db 472 AAGATT---GGGAAAAAGAAATGAAGAAAGCTATTTTATGGATTGTGGCAATTCAC 528
Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 529 GCAGAGATGGGTCTCCCGAGCATTTCTCCAGTGGTTGTTCTATCAGGCAACCAAACT 588
Qy 173 ----- 173
Db 589 TATGGGAGAAACAAATTTATGACCAAACTCTTGGACCGAATGAATTTTATCAITTTCTCT 648
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182
Db 649 GTGTTCAATGTTGATGATATATTTGGTCAATGACAAAGAACCCGATGTGGAGAAAAAT 708
Qy 183 ArgSerPheTyTrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202
Db 709 CGTTCAGAACCAAAACTCCAATGCATCGGCACTGACCTCAACAGGATTTT---AAT 765
Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyTrpCysGlyLeu 222
Db 766 GCTTCATGGAACCTCCATTCTCAACACCAATGACCCATGTGCAGATACTATCGGGGCTCT 825
Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
Db 826 GCACACAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTTCATTAGAACCCACTGAAT 885
Qy 243 GlnIleLysAlaTyrlleSerMetHisSerTySerGlnHisIleValPheProTyTrSer 262
Db 886 GAAATCAAGGTTTACATCACTTCCATTCTACTCCAGATGCTATTTGTTTCCCTATGGA 945
Qy 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
Db 946 TATACATCAAAACCTGCCACCTAACCATGTGGCTTGGCCAAAGTTGCAAGATTGGCACT 1005
Qy 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyThrHisGlyHisGlySerGluThr 302
Db 1006 GATGTTTCTTA---TCAACTCGATATGAAACCGCTGATACATCTATGGCCCAATAGATCAACA 1062
Qy 303 LeuTyTrLeuAlaProGlyGlyGlyAspTrpIleTyTrAspLeuGlyIleLysTySer 322
Db 1063 ATTTACCCGATATCAGGTTCTCTTTTAGATGGGCTTATGACCTGGGCGCATCAACACACA 1122
Qy 323 Phe 323
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Db 1123 TTT 1125
RESULT 12
US-10-229-546-1
; Sequence 1, Application US/10229546
; Publication No. US20030082649A1
; GENERAL INFORMATION:
; APPLICANT: Weich, Nadine S.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE
; FILE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
; FILE REFERENCE: MPI01-1561RNM
; CURRENT FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1254)
US-10-229-546-1
Alignment Scores:
Pred. No.: 3.58e-66 Length: 1622
Score: 622.00 Matches: 128
Percent Similarity: 55.12% Conservative: 71
Best Local Similarity: 35.46% Mismatches: 118
Query Match: 34.59% Indels: 44
DB: 14 Gaps: 7
US-09-980-881A-3 (1-338) x US-10-229-546-1 (1-1622)
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
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QY 21 GlnAsnLeuThrThrThrThrGluLeuValLeuProValThrAlaAspLeu 40
Db 121 AAGGACTTGGCCAAACCAATGAGTTCCTGCTGATCCAGGTGCCACCCACCGTA 180
QY 41 ValLysLysGlnValHisPheValAsnAlaSerValAspValLeuAla 60
Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGAAATCCCAAGCCATCCAGTCT 240
QY 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80
Db 241 GCCTTGATCAATAAATAATGACATGAAATCTTGATTCATGATCTACGAAGAAGATT 300
QY 81 GlnGlnGlnLeuSer---AsnAspThrValSerProArgAlaSerAlaSerTyrtTyrtGlu 99
Db 301 GAGAAACAGTTTGATGTTAAGAAGATATCCAGGAGGACACAGC-----TAGCA 351
QY 100 GlnTyHisSerLeuAsnGluLeuTyrtSerTrpLeuGluPheLeuThrGluArgHisPro 119
Db 352 AAATACAAATATTTGGGAAAAGATTTGGCTTGGACTGAAAAGATGATGATAAGTATCCT 411
QY 120 AspMetLeuThrLysLeuHisLeuGlySerPheGluLysTyrtProLeuTyrtValLeu 139
Db 412 GAATGCTCTCTGATTAATAATGATCTACTGTTGAGATTAATCCACTATATGTTCTG 471
QY 140 LysValSerGlyLysGlnThrAlaLysAsnAlaLeuTrpLeuAspCysGlyLeuHis 159
Db 472 AAGATT--GGGAAAAGATGAAGAAGAAAGCTATTTTATGATTTGGCAATTCAC 528
QY 160 AlaArgGluTrpLeuSerProAlaPheCysLeuTrpPheLeu----- 173
Db 529 GCACGAGATGGGTCTCCCGAGCATTTCTGCGAGTGGTGTTCCTATCAGGCAACCAAACT 588
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QY 173 ----- 173
Db 589 TATGGGAGAAACAAAATATATGACCAAACTCTTGGACCGAATGAATTTTACATTTCTCTCT 648
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Db 649 GTGTTCAATGTTGATGGATATATTTGGTCATGGACAAAGAACCGCATGTGGAGAAAAAT 708
QY 183 ArgSerPheTyrtAlaAsnHisCysLeuGlyThrAspLeuAsnArgPheAlaSer 202
Db 709 CGTTCCAAAGAACCAAAACTCCAAATGATCGGCACCTCAACAGGAATTTT--AAT 765
QY 203 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrtCysGlyLeu 222
Db 766 GCTTCATGGAACCTCCATTCCTAACACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825
QY 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnLeu 242
Db 826 GCACCAAGAGTCCGAGAAAGAGCAAGCTGTCACTAATTTCAATTATTAGAACCCACTGAAT 885
QY 243 GlnLeuLysAlaTyrtLeuSerMetHisSerTyrtSerGlnHisLeuValPheProTyrtSer 262
Db 886 GAAATCAAGTTTACATCACCTTCCATTCCTACTCCAGATGCTATTTTCCCTATGGA 945
QY 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
Db 946 TATACATCAAAACTGCCACCTAACCATGAGGACTTGGCCAAAGTTGCAAGATTGGCACT 1005
QY 283 ArgAlaLeuGluLysThrSerLysAsnThrArgTyrtThrHisGlyHisGlySerGluThr 302
Db 1006 GATGTTCTA---TCAACTCGATATGAACCCGCTACATCTATGGCCCAATAGAAATCAACA 1062
QY 303 LeuTyrtLeuAlaProGlyGlyAspAspTrpLeuTyrtAspLeuGlyLeuTyrtSer 322
Db 1063 ATTTACCCGATATCAGGTTCTCTTTAGACTGGGCTTATGACCTGGGCATCAAAACACACA 1122
QY 323 Phe 323
Db 1123 TTT 1125
RESULT 13
US-10-429-802-21
; Sequence 21, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSC:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; PRIOR FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-429-802-21
Alignment Scores:
Pred. No.: 3.58e-66 Length: 1622
Score: 622.00 Matches: 128
Percent Similarity: 55.12% Conservative: 71
Best Local Similarity: 35.46% Mismatches: 118
Query Match: 34.59% Indels: 44
DB: 15 Gaps: 7
US-09-980-881A-3 (1-338) x US-10-429-802-21 (1-1622)
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Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
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Db 61 TTTGACGAGGAGAGGTGTTCCCGGTGAAGCCCGCAGGATGAAACCAACGACGACATCAT 120
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Qy 21 GlnAsnLeuThrThrThrTyrrGluileValLeuTrpGlnProValThrAlaAspLeuile 40
    |||
Db 121 AAGGACTTGGCCAAACCAATGACTTGACTTCTGGTATCCAGGTGCCACCCACCGTA 180
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Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspValLysAla 60
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Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240
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Qy 61 HisLeuAsnValSerGlyileProCysSerValLeuLeuAlaAspValGluAspLeuile 80
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Db 241 GCCTTGGATCAAAATAAATGCATATGAAATCTTGATTCATGATCTACAAGAGAGATT 300
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Qy 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
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Db 301 GAGAACACAGTTTGATTTAAGAGAGATATCCAGCGCAGGCACAGC-----TACGCA 351
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Qy 100 GlnTyrHisSerLeuAsnGluileTyrSerTrpIleGluPheIleThrGluArgHisPro 119
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Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
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Db 412 GAAATGGTCTCTCGATTTAAATTTGGAATCTTGAATCTTGGTATCCAGGATATGTTCTG 471
    |||
Qy 140 LysValSerGlyLysGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
    |||
Db 472 AAGATT---GGGGAAGAGATGAAAGAGAAAGCTATTTTATGGATTGGGATTCAC 528
    |||
Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
    |||
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Qy 173 ----- 173
    |||
Db 589 TATGGGAGAAACAAATATGACCAAACTCTTGGACCGAATGAATTTTACATTCTTCCT 648
    |||
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182
    |||
Db 649 GTGTTCAATGTTGATGATATATTGTTGTCATGGACAAAGAACCCGATGTGGAGAAAT 708
    |||
Qy 183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhAlaSer 202
    |||
Db 709 CGTTCCAAAGAACCAAACTCCAAATGCATCGGCACCTGACCTCAACAGGAATTTT---AAT 765
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Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 222
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Db 766 GCTTCATGGAACTCCATTCCTTAACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825
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Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
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Db 826 GCACGAGAGTCGAGAGAGACGAAAGCTGTCTACTAATTTCAATAGAGCCACCTGAAT 885
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Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262
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Db 1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGCGCCCAATAGAATCAACA 1062
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Qy 303 LeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
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Qy 323 Phe 323
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Db 1123 TTT 1125
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RESULT 14
US-10-430-503-12
; Sequence 12, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAW-CHING
; APPLICANT: LAN, KENG-HSIN
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
; FILE REFERENCE: UTSC:797US
; CURRENT APPLICATION NUMBER: US/10/430,503
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/383,063
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-430-503-12

Alignment Scores:
Pred. No.: 3,58e-66 Length: 1622
Score: 622.00 Matches: 128
Percent Similarity: 55.12% Conservative: 71
Best Local Similarity: 35.46% Mismatches: 118
Query Match: 34.59% Indels: 44
DB: 16 Gaps: 7

US-09-980-881A-3 (1-338) x US-10-430-503-12 (1-1622)

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Qy 21 GlnAsnLeuThrThrThrTyrrGluileValLeuTrpGlnProValThrAlaAspLeuile 40
    |||
Db 121 AAGGACTTGGCCAAACCAATGACTTGACTTCTGGTATCCAGGTGCCACCCACCGTA 180
    |||
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspValLysAla 60
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Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240
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Qy 61 HisLeuAsnValSerGlyileProCysSerValLeuLeuAlaAspValGluAspLeuile 80
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Db 241 GCCTTGGATCAAAATAAATGCATATGAAATCTTGAATCTTGGTATCCAGGAGAGATT 300
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Qy 81 GlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99
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Db 301 GAGAACACAGTTTGATTTAAGAGAGATATCCAGCGCAGGCACAGC-----TACGCA 351
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Db 352 AAATACAAATAATTCGGAAGAGATTGTGCTTGGACTGAAAGAGATGATGGATAAGTATCCT 411
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Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139
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Db 412 GAAATGGTCTCTCGATTTAAATTTGGAATCTTGAATCTTGGTATCCAGGATATGTTCTG 471
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Qy 140 LysValSerGlyLysGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159
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Db 472 AAGATT---GGGGAAGAGATGAAAGAGAAAGCTATTTTATGGATTGGGATTCAC 528
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Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
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Qy 173 ----- 173
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Db 589 TATGGGAGAAACAAATATGACCAAACTCTTGGACCGAATGAATTTTACATTCTTCCT 648
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Qy 183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhAlaSer 202
    |||
Db 709 CGTTCCAAAGAACCAAACTCCAAATGCATCGGCACCTGACCTCAACAGGAATTTT---AAT 765
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Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 222
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Db 766 GCTTCATGGAACTCCATTCCTTAACCAATGACCCATGTGCAGATAACTATCGGGGCTCT 825
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Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242
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Db 826 GCACGAGAGTCGAGAGAGACGAAAGCTGTCTACTAATTTCAATAGAGCCACCTGAAT 885
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Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262
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Qy 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282
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Qy 283 ArgAlaIleGluLysSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302
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Db 1006 GATGTTCTA---TCAACTCGATATGAAACCCGCTACATCTATGCGCCCAATAGAATCAACA 1062
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Qy 303 LeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLysTyrSer 322
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Db 1063 ATTTACCGGATATCAGGTTCTTTTAGACTGGGCTTATGACCTGGGATCAACACACA 1122
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Qy 323 Phe 323
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:34:50 ; Search time 18.7627 Seconds  
(without alignments)  
869.503 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 1338  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1239.5	92.6	423	1	US-07-649-591B-3
3	1239.5	92.6	423	1	US-08-277-540-3
4	1239.5	92.6	423	1	US-08-430-787A-3
5	1239.5	92.6	423	2	US-08-869-057-2
6	1228.5	91.8	423	4	US-09-813-133A-4
7	610	45.6	307	2	US-08-782-760-6
8	610	45.6	307	5	PCT-US96-00995-6
9	582	43.5	306	1	US-08-696-139-4
10	582	43.5	404	1	US-09-011-769A-51
11	567	42.4	329	4	US-09-011-769A-47
12	567	42.4	349	4	US-08-860-882A-57
13	567	42.4	415	2	US-09-011-769A-39
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16	561	41.9	417	1	US-08-277-540-7
17	561	41.9	417	1	US-08-430-787A-7
18	561	41.9	417	1	US-09-011-769A-60
19	560	41.9	349	4	US-09-011-769A-64
20	559	41.8	349	4	US-07-649-591B-4
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22	554	41.4	396	1	US-08-430-787A-4
23	554	41.4	396	1	US-07-649-591B-6
24	552	41.3	417	1	US-08-277-540-6
25	552	41.3	417	1	US-08-430-787A-6
26	552	41.3	417	1	US-09-917-254-66
27	552	41.3	417	4	US-09-917-254-66

28	549	41.0	437	4	US-09-675-305-10	Sequence 10, Appl
29	549	41.0	437	4	US-10-200-344-10	Sequence 10, Appl
30	549	41.0	613	3	US-09-171-945-113	Sequence 113, App
31	549	41.0	716	3	US-09-171-945-125	Sequence 125, App
32	492	36.8	399	4	US-03-710-099-8	Sequence 8, Appli
33	492	36.8	399	4	US-10-200-910-8	Sequence 8, Appli
34	487.5	36.4	419	1	US-07-649-591B-5	Sequence 5, Appli
35	487.5	36.4	419	1	US-08-277-540-5	Sequence 5, Appli
36	487.5	36.4	419	1	US-08-430-787A-5	Sequence 5, Appli
37	483	36.1	417	1	US-07-649-591B-8	Sequence 8, Appli
38	483	36.1	417	1	US-08-277-540-8	Sequence 8, Appli
39	483	36.1	417	1	US-08-430-787A-8	Sequence 8, Appli
40	471.5	35.2	350	4	US-09-675-305-12	Sequence 12, Appl
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43	465.5	34.8	419	3	US-09-395-936-2	Sequence 2, Appli
44	465.5	34.8	436	4	US-09-710-099-6	Sequence 6, Appli
45	465.5	34.8	436	4	US-10-200-910-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinlu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813.133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-813-133A-2

Query Match	93.9%	Score 1257;	DB 4;	Length 386;
Best Local Similarity	99.1%	Pred. No. 1.4e-131;		
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Db	175	WIDCGIHAREWISPAFCINFIHNRMRKRSFYANNHCIGTDLNRNFASKHWCCEGASS	234	
Qy	121	SSCSETYCGLYPSEPEVKAVASFLRRNINQIKAYISMHSYSHIVFPYSTRSKSDHE	180	
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Qy	181	ELSVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT	232	
Db	295	ELSVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT	346	

RESULT 2  
US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/649,591B  
 FILING DATE: 19910201  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/266-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 423 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear

US-07-649-591B-3  
 Query Match 92.6%; Score 1239.5; DB 1; Length 423;  
 Best Local Similarity 86.2%; Pred. No. 1.4e-129;  
 Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60  
 Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 174  
 Qy 61 WIDCGIHAREWISPAFLWFIGH----- 83  
 Db 175 WIDCGIHAREWISPAFLWFIGHITQFYGIQYTNLLRLVDFYVMPVNVVDGYDSWKK 234  
 Qy 84 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 143  
 Db 235 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 294  
 Qy 144 FLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203  
 Db 295 FLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354  
 Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
 Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 3  
 US-08-277-540-3  
 ; Sequence 3, Application US/08277540  
 ; Patent No. 547901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 547901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 423 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-277-540-3  
 Query Match 92.6%; Score 1239.5; DB 1; Length 423;  
 Best Local Similarity 86.2%; Pred. No. 1.4e-129;  
 Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60  
 Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 174  
 Qy 61 WIDCGIHAREWISPAFLWFIGH----- 83  
 Db 175 WIDCGIHAREWISPAFLWFIGHITQFYGIQYTNLLRLVDFYVMPVNVVDGYDSWKK 234  
 Qy 84 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 143  
 Db 235 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 294  
 Qy 144 FLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203  
 Db 295 FLRRNINQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354  
 Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
 Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 4  
 US-08-430-787A-3  
 ; Sequence 3, Application US/08430787A  
 ; Patent No. 5593674  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430.787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-3

Query Match 92.6%; Score 1239.5; DB 1; Length 423;  
Best Local Similarity 86.2%; Pred. No. 1.4e-129;  
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVLVKSGKEQTAKNAI 60  
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVLVKSGKEQTAKNAI 174  
Qy 61 WIDCGIHAREWISPAFLWFIQH----- 83  
Db 175 WIDCGIHAREWISPAFLWFIQHITQFYGIIGQYTNLLRLVDFVMPVNVVDGYDSWKK 234  
Qy 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSSCSETYCGLYPSEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSSCSETYCGLYPSEPEVKAVAS 294  
Qy 144 FLRRNIQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 295 FLRRNIQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 5  
US-08-869-057-2  
Sequence 2, Application US/08869057  
Patent No. 5985562  
GENERAL INFORMATION:  
APPLICANT: Morser, Michael J  
APPLICANT: Nagashima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue

CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
TISSUE TYPE: Plasma  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 23..401  
US-08-869-057-2

Query Match 92.6%; Score 1239.5; DB 2; Length 423;  
Best Local Similarity 86.2%; Pred. No. 1.4e-129;  
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVLVKSGKEQTAKNAI 60  
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVLVKSGKEQTAKNAI 174  
Qy 61 WIDCGIHAREWISPAFLWFIQH----- 83  
Db 175 WIDCGIHAREWISPAFLWFIQHITQFYGIIGQYTNLLRLVDFVMPVNVVDGYDSWKK 234  
Qy 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSSCSETYCGLYPSEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSSCSETYCGLYPSEPEVKAVAS 294  
Qy 144 FLRRNIQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 295 FLRRNIQIKAYISMHSYSQHIYFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 6  
US-09-813-133A-4  
Sequence 4, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinlu et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match      91.8%; Score 1228.5; DB 4; Length 423;
Best Local Similarity 85.5%; Pred. No. 2.4e-128;
Matches 230; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

Oy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQAANKAI 174
Oy 61 WIDCGIHAREWISPAFLWFTGH-----GH----- 83
Db 175 WIDCGIHAREWISPAFLWFTGHITQFYGIICQVNTLLRLVDFYVMPVNVVDGYDSWKK 234
Oy 84 NRMWRKNSFYANNHCIGTDLRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVAS 143
Db 235 NRMWRKNSFYANNHCIGTDLRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVAS 294
Oy 144 FLRRNINQIKAYISMHSYSQHIYVPPYSYTRSKSKDHELSIVASEAVRAIEKTSKNTRYT 203
Db 295 FLRRNINQIKAYISMHSYSQHIYVPPYSYTRSKSKDHELSIVASEAVRAIEKTSKNTRYT 354
Oy 204 HGHGETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 HGHGETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 7
US-08-782-760-6
; Sequence 6, Application US/08782760
; Patent No. 5948668
; GENERAL INFORMATION:
; APPLICANT: Hartman, Jacob
; APPLICANT: Fulga, Netta
; APPLICANT: Mendelovitch, Simona
; APPLICANT: Gorecki, Marian
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid

; SEQ ID NO 5
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-08-782-760-6

Query Match      45.6%; Score 610; DB 2; Length 307;
Best Local Similarity 45.0%; Pred. No. 1.6e-59;
Matches 121; Conservative 43; Mismatches 65; Indels 40; Gaps 5;

Oy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60
Db 1 ASGHSYTKYNNWETIEAWIQQVATDNDPLVTQSVIGTTFEGRNNMYLKI-GKTRPNKPAI 59
Oy 61 WIDCGIHAREWISPAFLWFI-----GH----- 83
Db 60 FIDCGFHAREWISPAFCQFVREAVRTYNOEIHMKQLLDLDFVLPVNVIDGVVYVTK 119
Oy 84 NRMWRKNSFYANNHCIGTDLRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVAS 143
Db 120 DRMRKTRSTMAGSSCLGVDPNRNF-NA3WCEVGASRSPCSETYCGPAPESEKETKALAD 178
Oy 144 FLRRNINQIKAYISMHSYSQHIYVPPYSYTRSKSKDHELSIVASEAVRAIEKTSKNTRYT 203
Db 179 FIRNLSITIKAYLTIHSYSQWMLYPYSYQYKLPENYBELNALVKGAAKEL-ATLHGTYKT 237
Oy 204 HGHSETLYLAPGGDDWIYDLGIKYSFT 232
Db 238 YPGATTIYPAGGSDWSDYDQGIKYSFT 266

RESULT 8
PCT-US96-00995-6
; Sequence 6, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00995-6

Query Match      45.6%; Score 610; DB 5; Length 307;
Best Local Similarity 45.0%; Pred. No. 1.6e-59;
Matches 121; Conservative 43; Mismatches 65; Indels 40; Gaps 5;

Oy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60
```

Db 1 ASGHSYTKYNWETIAMIQQVATDNDPLVTQSVIGTTFEGNNMYLKI-GKTRPNKPAI 59  
Qy 61 WIDCGIHAREWISPAFCLEFI-----GH----- 83  
Db 60 FIDCGFHAREWISPAFCQMFVREAVRTYQBIHMKQLDELDFVLPVNNIDGVVYTWTK 119  
Qy 84 NRMKRNRSFYANNHCIGTDLNRFNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVAS 143  
Db 120 DRMKRTRSTWAGSSCLGVDPNRF-NAGWCEVGASRSPCSETYCGPAPESKEKETKALAD 178  
Qy 144 FLRNINQIKAYISMHSYSQIHVFPYSYTRSKSDHELSLVSBAVRAIEKTSKNTRYT 203  
Db 179 FIRNLSITIKAYLTHSYQMLYPYSYDYKLPENYBELNALVGAAKEL-ATLHGTYT 237  
Qy 204 HGHGSETLYLAPGGDDMIYDLGIKYSET 232  
Db 238 YPGGATTYPAAGGSDMSYDQGIKYSET 266

## RESULT 9

US-08-696-139-4  
; Sequence 4, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hersberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 306 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-696-139-4

Query Match 43.5%; Score 582; DB 1; Length 306;  
Best Local Similarity 44.3%; Pred. No. 2.28-56;  
Matches 117; Conservative 40; Mismatches 67; Indels 40; Gaps 5;

Qy 6 YEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSPEKYPYLVKVSQKQAKNAIWDCG 65

Db 6 YEKYNWETIEAWTKQVTSNPOLISRTAIGTTFLGNNIYLLKY-GKPGPNKPAIFMDCG 64  
Qy 66 IHAREWISPAFCLEFI-----GH-----NRMWR 88  
Db 65 FHAREWISPAFCQMFVREAVLTGYESHMTFELNKLDFYVLPVLNIDGIYITWTKNRMWR 124  
Qy 89 KNRSFYANNHCIGTDLNRFNPFASKHWCCEGASSSSCSETYCGLYPESEPEVKAVASFLRRN 148  
Db 125 KTRSTWAGTTCIGTDPNRF-DAGWCTTGASTPCDETYCGSAAESEKETKALADFIINN 183  
Qy 149 INQIKAYISMHSYSQIHVFPYSYTRSKSDHEELSLVSBAVRAIEKTSKNRTRTHGHGS 208  
Db 184 LSSIKAYLTHSYQMLYPYSYDYKLPENNAELNLAKAAVKEL-ATLYGTYKTYGPGA 242  
Qy 209 ETLYLAPGGDDMIYDLGIKYSET 232  
Db 243 TTIYPAAGGSDMWAYDQGIKYSET 266

## RESULT 10

US-08-696-139-2  
; Sequence 2, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hersberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 404 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-696-139-2

Query Match 43.5%; Score 582; DB 1; Length 404;  
Best Local Similarity 44.3%; Pred. No. 3.3e-56;  
Matches 117; Conservative 40; Mismatches 67; Indels 40; Gaps 5;

Qy 6 YEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSPEKYPYLVKVSQKQAKNAIWDCG 65

Db 104 YEKNNWETIEAWTKQVTSNPDLISRTAIGTFLGNNIYLLKV-GKPGPKPAIFWDCG 162  
Qy 66 IHAREWISPAFLWFI-----GH-----NRMR 88  
Db 163 PHAREWISHAFQWFRVAVLTGYESHMTBFLNLDFFVLPVLNIDGIYIYTWKMR 222  
Qy 89 KNRFYANNHICIGTDLNRFASKHWCBSGSSCSEYCYGLYPSEPEVKAVASFLRN 148  
Db 223 KTRSTNAGTTCIGTDPNRNF-DAGWCTTGASTDPCDETYCGSAAESEKETKALADIRNN 281  
Qy 149 INQIKAYISMSYSHIYVPPSYTRSKSDHEELSLVASEAVRALEKTSKNTRYTHGHS 208  
Db 282 LSSIKAYITHSYQMLIPYSYDYKLPENNAELNLAKAAVKEL-ATLYGTYTYGPA 340  
Qy 209 ETLYLAPGGDDWIYDLGIKYSFT 232  
Db 341 TTIYPAAGSDDWAYDQIKYSFT 364

## RESULT 11

US-09-011-769A-51  
; Sequence 51, Application US/09011769A  
; Patent No. 6436691

## GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.

## TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995

## INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-011-769A-51

Query Match 42.4%; Score 567; DB 4; Length 329;  
Best Local Similarity 41.3%; Pred. No. 1.1e-54;  
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQVHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEKYPLYVLKVSQKQAKNAI 60

Db 23 ATGSHYKYNKWETIEAWTQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 81  
Qy 61 WIDCGIHAREWISPAFLWFI-----GH-----83  
Db 82 FMDGPHAREWISPAFLWFI-----GH-----141  
Qy 84 NRMWRKRSYANNHICIGTDLNRFASKHWCBSGSSCSEYCYGLYPSEPEVKAVAS 143  
Db 142 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCEDETYCGPAABSEKETKALAD 200  
Qy 144 FLERNINOIKAYISMSYSHIYVPPSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 201 FIRNKLSSIKAYLTIHSYQMLIPYSYAYKLGENNAELNALAKATYKEL-ASLHGTYKT 259  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 260 YGPGATTIYPAAGSDDWAYDQGIYSFT 288

## RESULT 12

US-09-011-769A-47  
; Sequence 47, Application US/09011769A  
; Patent No. 6436691

## GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.

## TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995

## INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:  
LENGTH: 349 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-011-769A-47

Query Match 42.4%; Score 567; DB 4; Length 349;  
Best Local Similarity 41.3%; Pred. No. 1.2e-54;  
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQVHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEKYPLYVLKVSQKQAKNAI 60



Db 23 ATGSEYKYNKWEIEATWTOQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 81  
Qy 61 WIDCGIHAREWISPAFLWFI-----GH----- 83  
Db 82 FMDGCFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFVLPVLNIDGYIYTWTK 141  
Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCESGASSSCSETYCGLYPSEPEVKAVAS 143  
Db 142 SRFWRKTRSTHTGSSCIGTDNRNF-DAGWCEIGASRNPCEYCGPAASEKETKALAD 200  
Qy 144 FLRNINQIKAYISMHSYQHIYVPYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 201 FIRKLSSIKAYLTIHSYQMMIYPSYAYKLGENNAELNALAKATVKEL-ASLHGKTYT 259  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 260 YGPGATTIYPAGGDDWAYDQGIYSFT 288

## RESULT 13

US-08-860-882A-57  
; Sequence 57, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGLESE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HOW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-860-882A-57

Query Match 42.4%; Score 567; DB 2; Length 415;  
Best Local Similarity 41.3%; Pred. No. 1.6e-54;  
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQYHSLNIEYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGKEQAKNAI 60  
Db 109 ATGSEYKYNKWEIEATWTOQVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 167  
Qy 61 WIDCGIHAREWISPAFLWFI-----GH----- 83  
Db 168 FMDGCFHAREWISPAFCQWFVREAVRTYGREIQVTELLDKLDFVLPVLNIDGYIYTWTK 227  
Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCESGASSSCSETYCGLYPSEPEVKAVAS 143  
Db 228 SRFWRKTRSTHTGSSCIGTDNRNF-DAGWCEIGASRNPCEYCGPAASEKETKALAD 286  
Qy 144 FLRNINQIKAYISMHSYQHIYVPYSYTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 287 FIRKLSSIKAYLTIHSYQMMIYPSYAYKLGENNAELNALAKATVKEL-ASLHGKTYT 345  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 346 YGPGATTIYPAGGDDWAYDQGIYSFT 374

## RESULT 14

US-09-011-769A-39  
; Sequence 39, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; APPLICANT: BLAKEY, David C.  
; APPLICANT: DAVIES, David H.  
; APPLICANT: HENNAM, John F.  
; APPLICANT: HENNEQUIN, Laurent F.A.  
; APPLICANT: MARSHAM, Peter R.  
; APPLICANT: DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-011-769A-39

Query Match 42.4%; Score 567; DB 4; Length 415;  
Best Local Similarity 41.3%; Pred. No. 1.6e-54;  
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSKEQTAKNAI 60  
Db 109 ATGHSYEKYNKWETIEAWTQOVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 167  
Qy 61 WIDCGIHAREWISPAFLWFI-----GH----- 83  
Db 168 FMDCGFHAREWISPAFCWFVREAVRTYGRIGTQVTELLDKLDFVLPVNLIDGYIYTWTk 227  
Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKWCEBEGASSSSCSETYCGLYPSEPEVKAVAS 143  
Db 228 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETTCGPAASEKETKALAD 286  
Qy 144 FLRNINQIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAJEKTSKNTRYT 203  
Db 287 FIRKLSSIKAYLTIHSYQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTYT 345  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 346 YGPGATTIYPAGGSDWAYDQGIYSFT 374

RESULT 15

US-09-011-769A-56  
; Sequence 56, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-011-769A-56

Query Match 42.4%; Score 567; DB 4; Length 424;  
Best Local Similarity 41.3%; Pred. No. 1.7e-54;  
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKYPLYVLKVSKEQTAKNAI 60  
Db 118 ATGHSYEKYNKWETIEAWTQOVATENPALISRSVIGTTFEGRAIYLLKV-GKAGQNKPAI 176  
Qy 61 WIDCGIHAREWISPAFLWFI-----GH----- 83  
Db 177 FMDCGFHAREWISPAFCWFVREAVRTYGRIGTQVTELLDKLDFVLPVNLIDGYIYTWTk 236  
Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKWCEBEGASSSSCSETYCGLYPSEPEVKAVAS 143  
Db 237 SRFWRKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETTCGPAASEKETKALAD 295  
Qy 144 FLRNINQIKAYISMHSYSOHIVFPYSYTRSKSKDHEELSLVASEAVRAJEKTSKNTRYT 203  
Db 296 FIRKLSSIKAYLTIHSYQMMIYPYSYAYKLGENNAELNALAKATVKEL-ASLHGTYT 354  
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
Db 355 YGPGATTIYPAGGSDWAYDQGIYSFT 383

Search completed: October 28, 2004, 19:47:10  
Job time : 25.7627 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 19:43:44 ; Search time 56.2881 Seconds  
(without alignments)  
1416.943 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 1338  
Sequence: 1 ASASYEQVHSLNEIYSWIE.....IKYFTSNPPVEXLLPLSLK 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	93.9	386	9	US-09-813-133A-2
2	1257	93.9	386	14	US-10-212-877-2
3	1239.5	92.6	423	14	US-10-379-836-17
4	1228.5	91.8	423	9	US-09-813-133A-4
5	1228.5	91.8	423	14	US-10-212-877-4
6	1216	90.9	428	15	US-10-115-479-68
7	1216	90.9	428	15	US-10-115-479-70
8	1164.5	87.0	423	14	US-10-379-836-2
9	1105.5	82.6	422	14	US-10-379-836-18
10	1095.5	81.9	422	14	US-10-379-836-16
11	837	62.6	322	15	US-10-115-479-64
12	816.5	61.0	211	9	US-09-925-302-467
13	816.5	61.0	211	10	US-09-925-302-467

14	798	59.6	354	15	US-10-115-479-66	Sequence 66, Appl
15	582	43.5	416	15	US-10-074-978A-269	Sequence 269, App
16	578	43.2	416	15	US-10-074-978A-270	Sequence 270, App
17	567	42.4	402	14	US-10-379-836-20	Sequence 20, Appl
18	567	42.4	417	15	US-10-074-978A-267	Sequence 267, App
19	567	42.4	417	15	US-10-074-978A-268	Sequence 268, App
20	567	42.4	417	16	US-10-477-515-3	Sequence 3, Appl1
21	552	41.3	417	14	US-10-229-546-2	Sequence 2, Appl1
22	552	41.3	417	14	US-10-229-546-9	Sequence 9, Appl1
23	552	41.3	417	14	US-10-341-434-188	Sequence 188, App
24	552	41.3	417	15	US-10-262-511-72	Sequence 72, Appl
25	550.5	41.1	374	9	US-09-888-615-61	Sequence 61, Appl
26	550.5	41.1	444	14	US-10-176-306-74	Sequence 2, Appl1
27	549	41.0	434	13	US-10-477-515-2	Sequence 10, Appl
28	549	41.0	437	13	US-10-200-344-10	Sequence 12, Appl
29	549	41.0	437	14	US-10-274-639-12	Sequence 12, Appl
30	549	41.0	437	15	US-10-333-574-12	Sequence 12, Appl
31	549	41.0	613	9	US-09-910-059-113	Sequence 125, App
32	549	41.0	613	16	US-10-608-710-4	Sequence 4, Appl1
33	549	41.0	716	9	US-09-910-059-125	Sequence 125, App
34	547.5	40.9	416	15	US-10-074-978A-266	Sequence 266, App
35	547	40.9	437	17	US-10-757-262-128	Sequence 128, App
36	530	39.6	286	15	US-10-072-012-887	Sequence 887, App
37	519	38.8	286	16	US-10-408-765A-1959	Sequence 1959, Ap
38	502.5	37.6	419	15	US-10-072-012-788	Sequence 788, App
39	501.5	37.5	298	14	US-10-379-836-19	Sequence 19, Appl
40	492	36.8	399	14	US-10-200-910-8	Sequence 8, Appl1
41	492	36.8	399	17	US-10-843-130-8	Sequence 8, Appl1
42	488.5	36.5	419	15	US-10-072-012-787	Sequence 787, App
43	471.5	35.2	350	13	US-10-200-344-12	Sequence 12, Appl
44	465.5	34.8	406	9	US-09-925-297-517	Sequence 517, App
45	465.5	34.8	419	14	US-10-345-680-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: US\$ THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match	93.9%	Score	1257;	DB	9;	Length	386;
Best Local Similarity	99.1%	Pred. No.	5.1e-121;				
Matches	230;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
Qy	1	ASASYEQVHSLNEIYSWIEFITERPDMLT	KIHGSSFEKYPYLVYLVKVSQKEQTAKNAI	60			
Db	115	ASASYEQVHSLNEIYSWIEFITERPDMLT	KIHGSSFEKYPYLVYLVKVSQKEQAQNAI	174			
Qy	61	WIDCGIHAREWISPAFLMFI	GHNRMWRKVRSYANNHCITGTDLNRNFASKHCEGASS	120			
Db	175	WIDCGIHAREWISPAFLMFI	GHNRMWRKVRSYANNHCITGTDLNRNFASKHCEGASS	234			
Qy	121	SSCSEYTCGLYPSEPEVKAVASFL	RNINQIKAYISMSHSQHIYVPYTSKSKDHE	180			
Db	235	SSCSEYTCGLYPSEPEVKAVASFL	RNINQIKAYISMSHSQHIYVPYTSKSKDHE	294			

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Qy 181 ELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 295 ELSLVASAVRAIEKISKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 346

RESULT 2
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-877-2

Query Match 93.9%; Score 1257; DB 14; Length 386;
Best Local Similarity 99.1%; Pred. No. 5.1e-121;
Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 174

Qy 61 WIDCGIHAREWISPAFLWFIH-----
Db 175 WIDCGIHAREWISPAFLWFIHITQFY3IIGQYTNLLRLVDFVMPVNVVDGYDSWKK 234

Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 143
Db 235 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 294

Qy 144 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 295 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-836-17

Query Match 92.6%; Score 1239.5; DB 14; Length 423;
Best Local Similarity 86.2%; Pred. No. 3.7e-119;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

Qy 181 ELSLVASAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 295 ELSLVASAVRAIEKISKNTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 346

RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-836-17

Query Match 92.6%; Score 1239.5; DB 14; Length 423;
Best Local Similarity 86.2%; Pred. No. 3.7e-119;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;
```

```
Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 174

Qy 61 WIDCGIHAREWISPAFLWFIH-----
Db 175 WIDCGIHAREWISPAFLWFIHITQFY3IIGQYTNLLRLVDFVMPVNVVDGYDSWKK 234

Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 143
Db 235 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 294

Qy 144 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 295 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCS THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match 91.8%; Score 1228.5; DB 9; Length 423;
Best Local Similarity 85.5%; Pred. No. 5.1e-118;
Matches 230; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSQKQAKNAI 174

Qy 61 WIDCGIHAREWISPAFLWFIH-----
Db 175 WIDCGIHAREWISPAFLWFIHITQFY3IIGQYTNLLRLVDFVMPVNVVDGYDSWKK 234

Qy 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 143
Db 235 NRMWRKRSFYANNHCIGTDLNRNFASKHWCEEGASSSSCSEYTCGLYPESEPEVKAVAS 294

Qy 144 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 295 FLRRNIQIKAYISMHSYQHIHVPYSTRSKKDHEELSLVASEAVRAIEKTSKNTRYT 354

Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
```

;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
;; TITLE OF INVENTION: USES THEREOF  
;; FILE REFERENCE: CL001173DIV  
;; CURRENT APPLICATION NUMBER: US/10/212,877  
;; PRIOR FILING DATE: 2002-08-07  
;; PRIOR APPLICATION NUMBER: 09/813,133  
;; PRIOR FILING DATE: 2001-03-21  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 4  
;; LENGTH: 423  
;; TYPE: PRT  
;; ORGANISM: Human  
US-10-212-877-4

Query Match 91.8%; Score 1228.5; DB 14; Length 423;  
Best Local Similarity 85.5%; Pred. No. 5.1e-118; Indels 37; Gaps 1;  
Matches 230; Conservative 0; Mismatches 2;  
QY 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSKEQTAKNAI 60  
DB 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKVSKEQAANKNAI 174  
QY 61 WIDCGIHAREWISPAFLWFIGH----- 83  
DB 175 WIDCGIHAREWISPAFLWFIGHITQFYGIQYTNLLRLVDFYVMPVNVVDGYDSWKK 234  
QY 84 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSCSETYCGLYPSEPEVKAVAS 143  
DB 235 NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSCSETYCGLYPSEPEVKAVAS 294  
QY 144 FLRRNIQIKAYISMHSYSQHVFPYSYTRSKSKDHBEELSLVASEAVRAIEKTSKNTRYT 203  
DB 295 FLRRNIQIKAYISMHSYSQHVFPYSYTRSKSKDHBEELSLVASEAVRAIEKTSKNTRYT 354  
QY 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
DB 355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383

## RESULT 6

US-10-115-479-68  
; Sequence 68, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:

; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malvanter, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann

;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

;; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
;; CURRENT APPLICATION NUMBER: US/10/115,479  
;; PRIOR FILING DATE: 2002-11-18  
;; PRIOR APPLICATION NUMBER: 60/281,136  
;; PRIOR FILING DATE: 2001-04-03  
;; PRIOR APPLICATION NUMBER: 60/281,863  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/281,906  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/282,934  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 68  
;; LENGTH: 428  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-115-479-68

Query Match 90.9%; Score 1216; DB 15; Length 428;  
Best Local Similarity 83.9%; Pred. No. 1e-116; Indels 42; Gaps 2;  
Matches 230; Conservative 0; Mismatches 2;  
QY 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVK-----VSGKEQT 55  
DB 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPYLVKGFPEQVSGKEQA 174  
QY 56 AKNAIWDGCIHAREWISPAFLWFIGH----- 83  
DB 175 AKNAIWDGCIHAREWISPAFLWFIGHITQFYGIQYTNLLRLVDFYVMPVNVVDGYD 234  
QY 84 -----NRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSCSETYCGLYPSEPEV 138  
DB 235 YSWKKNRMWRKNRSFYANNHCIGTDLNRNPFASKHWCCEGASSSCSETYCGLYPSEPEV 294  
QY 139 KAVASFLRRNIQIKAYISMHSYSQHVFPYSYTRSKSKDHBEELSLVASEAVRAIEKTSK 198  
DB 295 KAVASFLRRNIQIKAYISMHSYSQHVFPYSYTRSKSKDHBEELSLVASEAVRAIEKISK 354  
QY 199 NTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232  
DB 355 NTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 388

## RESULT 7

US-10-115-479-70  
; Sequence 70, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:

; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;

```
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Raetelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 70
/ LENGTH: 428
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-115-479-70
```

```
Query Match 90.9%; Score 1216; DB 15; Length 428;
Best Local Similarity 83.9%; Pred. No. 1e-116;
Matches 230; Conservative 0; Mismatches 2; Indels 42; Gaps 2;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLK-----VSGKEQT 55
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKGFPEQVSGKEQA 174
Qy 56 AKNAIWDGCIHAREWISPAFLWFIH----- 83
Db 175 AKNAIWDGCIHAREWISPAFLWFIHQFYGIIGQYTNLLRLVDFYVMPVNVVDCYD 234
Qy 84 -----NRWKRNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSETYCGLYPESPEV 138
Db 235 YSWKKNRNRNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSETYCGLYPESPEV 294
Qy 139 KAVASFLRRNIQIKAYISMHSYSHQIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSK 198
Db 295 KAVASFLRRNIQIKAYISMHSYSHQIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKISK 354
Qy 199 NTRYTHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 NTRYTHGSETLYLAPGGDDWIYDLGIKYSFT 388

RESULT 8
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```
US-10-379-836-2
/ Sequence 2, Application US/10379836
/ Publication No. US20030215850A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
/ TITLE OF INVENTION: TAFI
/ FILE REFERENCE: D0214NP
/ CURRENT APPLICATION NUMBER: US/10/379,836
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: U.S. 60/361,523
/ PRIOR FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 423
/ TYPE: PRT
/ ORGANISM: Papio hamadryas
US-10-379-836-2

Query Match 87.0%; Score 1164.5; DB 14; Length 423;
Best Local Similarity 80.7%; Pred. No. 2.1e-111;
Matches 217; Conservative 7; Mismatches 8; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGSKQETAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEITEKYPDMLTKIHGSSFEKHPLYVLKVGSKQETAKNAM 174
Qy 61 WIDCGIHAREWISPAFLWFIH----- 83
Db 175 WIDCGIHAREWISPAFLWFIHTEYGIIGETVNLRRHVDYVMPVNVVGVYDSWKK 234
Qy 84 NRWKRNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSETYCGLYPESPEVKAVAS 143
Db 235 NRWKRNRSFYANNRCIGTDLNRFASKHWCCEGASSSCSETYCGLYPESPEKAVAN 294
Qy 144 FLRRNIQIKAYISMHSYSHQIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 295 FLRRNIQIKAYISMHSYSHQIIVFPYSYTRSKSKDHEELSLVASEAVRAIQKTSKNIRYT 354
Qy 204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 355 HGRGSETLYLAPGGADDWIYDLGIKYSFT 383

RESULT 9
US-10-379-836-18
/ Sequence 18, Application US/10379836
/ Publication No. US20030215850A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
/ TITLE OF INVENTION: TAFI
/ FILE REFERENCE: D0214NP
/ CURRENT APPLICATION NUMBER: US/10/379,836
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: U.S. 60/361,523
/ PRIOR FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 18
/ LENGTH: 422
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-379-836-18

Query Match 82.6%; Score 1105.5; DB 14; Length 422;
Best Local Similarity 77.0%; Pred. No. 2.6e-105;
Matches 207; Conservative 10; Mismatches 15; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGSKQETAKNAI 60
Db 114 ASASYEQYHSLNEIYSWIEITEQHPDMLQKIYIGSSFEEKPLYVLKVGSKQETAKNAI 173
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Qy 61 WIDCGIHAREWISPAFLWFIQH----- 83
Db 174 WIDCGIHAREWISPAFLWFIQYVTFHGKENVYTRLLRHVDVYIMPVMNVGDYDWTWK 233
Qy 84 NRMWRKRSFYANNHCITGLNRNPFASKHWCCEGASSSCSETCYGLYPSEPEVKAVAS 143
Db 234 NRMWRKRSAHKNNRCVGTDLNRNPFASKHWCCEGASSSCSETCYGLYPSEPEVKAVAD 293
Qy 144 FLRRNINIKAYISMHSYSQIHVPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 294 FLRRNIDHIKAYISMHSYSQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYT 353
Qy 204 HGHGSETLYLAPGGDDMIYDLGIKYSFT 232
Db 354 HGSSESILYAPGGDDMIYDLGIKYSFT 382

RESULT 10
US-10-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Query Match 81.9%; Score 1095.5; DB 14; Length 422;
Best Local Similarity 75.8%; Pred. No. 2.8e-104;
Matches 204; Conservative 11; Mismatches 17; Indels 37; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGSKQETAKNAI 60
Db 114 ASSSYEQYHSLNEIYSWIEVITEQHPDMLQKIVIGSSYEKYPLYVLKVGSKHEHVZNAI 173
Qy 61 WIDCGIHAREWISPAFLWFIQH----- 83
Db 174 WIDCGIHAREWISPAFLWFIQYVTFHGKENVYTRLLRHVDVYIMPVMNVGDYDWTWK 233
Qy 84 NRMWRKRSFYANNHCITGLNRNPFASKHWCCEGASSSCSETCYGLYPSEPEVKAVAS 143
Db 234 NRMWRKRSVHMNNRCVGTDLNRNPFASKHWCCEGASSSCSETCYGLYPSEPEVKAVAD 293
Qy 144 FLRRNINIKAYISMHSYSQIHVPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 294 FLRRNINIKAYISMHSYSQILFPYSYNRSKSKDHEELSLVASEAVRAIESINKNTRYT 353
Qy 204 HGHGSETLYLAPGGDDMIYDLGIKYSFT 232
Db 354 HGSSESILYAPGGDDMIYDLGIKYSFT 382

RESULT 11
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
```

```
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Query Match 62.6%; Score 837; DB 15; Length 322;
Best Local Similarity 71.6%; Pred. No. 1e-77;
Matches 166; Conservative 0; Mismatches 2; Indels 64; Gaps 1;

Qy 1 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGSKQETAKNAI 60
Db 115 ASASYEQYHSLNEIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVGSKQAKNAI 174
Qy 61 WIDCGIHAREWISPAFLWFIQHNRWRKRSFYANNHCITGLNRNPFASKHWCCEGASS 120
Db 175 WID----- 177
Qy 121 SSCSETCYGLYPSEPEVKAVASFLRRNINIKAYISMHSYSQIHVPYSYTRSKSKDHE 180
Db 178 -----CGLYPESEPEVKAVASFLRRNINIKAYISMHSYSQIHVPYSYTRSKSKDHE 230
Qy 181 ELSLVASEAVRAIEKTSKNTRYTHGHGSETLYLAPGGDDMIYDLGIKYSFT 232
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Db 231 ELSLVASEAVRAIEKISKNTYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 282

RESULT 12

US-09-925-302-467

; Sequence 467, Application US/09925302

; Patent No. US20020044941A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 467

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-925-302-467:

Query Match 61.0%; Score 816.5; DB 9; Length 211;

Best Local Similarity 90.6%; Pred. No. 7.6e-76;

Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 71 WISPAFCLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCCEGASSS 122

Db 3 WIS-MLCRWLMMVMNYSKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCCEGASSS 61

QY 123 CSETYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSTRSKSDHEEL 182

Db 62 CSETYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSTRSKSDHEEL 121

QY 183 SLVASEAVRAIEKISKNTYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232

Db 122 SLVASEAVRAIEKISKNTYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 13

US-09-925-302-467

; Sequence 467, Application US/09925302

; Patent No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 467

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-925-302-467:

Query Match 61.0%; Score 816.5; DB 10; Length 211;

Best Local Similarity 90.6%; Pred. No. 7.6e-76;

Matches 154; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 71 WISPAFCLWFI-----GHNRMWRKNRSFYANNHCIGTDLNRNFASKHWCCEGASSS 122

Db 3 WIS-MLCRWLMMVMNYSKKNRMWRKNRSFYANNHCIGTDLNRNFASKHWCCEGASSS 61

QY 123 CSETYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSTRSKSDHEEL 182

Db 62 CSETYGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHIVFPYSTRSKSDHEEL 121

QY 183 SLVASEAVRAIEKISKNTYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232

Db 122 SLVASEAVRAIEKISKNTYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 14

US-10-115-479-66

; Sequence 66, Application US/10115479

; Publication No. US20040006205A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Miller, Charles E.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Zhong, Haihong

; APPLICANT: Smithson, Glendda

; APPLICANT: Casman, Stacie J.

; APPLICANT: Boldog, Ferenc L.;

; APPLICANT: Voss, Edward

; APPLICANT: Vernet, Corine

; APPLICANT: MacDougall, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei

; APPLICANT: Mezes, Peter S.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Patturajan, Meera E.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Malyanker, Uriel M.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-322 B (Cura 622 PT)

; CURRENT APPLICATION NUMBER: US/10/115,479

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 60/281,136

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/281,906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283,657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,234

; PRIOR FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: 60/285,325

; PRIOR FILING DATE: 2001-04-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 198

; SEQ ID NO 66

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-115-479-66

Query Match 59.6%; Score 793; DB 15; Length 354;



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Best Local Similarity 57.3%; Pred. No. 1.3e-73;
Matches 157; Conservative 0; Mismatches 1; Indels 116; Gaps 3;

Qy 1 ASASYEQYSLNLIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLK-----VSGKEQT 55
Db 115 ASASYEQYSLNLIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKPFPEQVSGKEQA 174
Qy 56 AKNAIWDICGHAREWISPAFLWFIGH-----83
Db 175 AKNAIWDICGHAREWISPAFLWFIGHITQFYGIQGYTNLLRLVDFYVMPVNVVDGYD 234
Qy 84 -----NRMWRKNRFRYANNHCIGTDLNRNFASKHWCBEGASSSCSSETYCGLYPESPEV 138
Db 235 YSWKKNRMRKNRFRYANNHCIGTDLNRNFASKHWCBEGASSSCSSETYCGLYPE-----289
Qy 139 KAVASFLRRNINQIKAYISMHSYSQHVPPYSYTRSKSKDHEELSLVASEAVRAIEKTSK 198
Db 290 -----289

Qy 199 NTRYTHGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db 290 -----SETLYLAPGGDDWIYDLGIKYSFT 314

RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Heriman, John
; APPLICANT: Pena, Carol B A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-074-978A-269

Query Match 43.5%; Score 582; DB 15; Length 416;
Best Local Similarity 44.3%; Pred. No. 3.3e-51;
Matches 117; Conservative 40; Mismatches 67; Indels 40; Gaps 5;

Qy 6 YEQYHSLNLIYSWIEFITERHPDMLTKIHGSSFEKYPLYVLKVSQKEQTAKNAIWIDCG 65
Db 116 YEKNNWETIEATWKQVTSNPDLISRTAIGTTFGLGNVIYLLKV-GKPGPNKPAIFMDCG 174
Qy 66 IHAREWISPAFLWFI-----GH-----NRMWR 88
Db 175 FHAREWISHAFQCFVREAVLTYGESHMTFLNKLDFVLPVLNIDGYIYTWTKNRMWR 234
Qy 89 KRSFYANNHCIGTDLNRNFASKHWCBEGASSSCSSETYCGLYPESEPEVKAVASFLRN 148
Db 235 KTRSTNAGTTCIGTDPNRF-DAGWCTTGASTDPCDETYCGSAAESEKETKALADFIRNN 293
Qy 149 INQIKAYISMHSYSQHVPPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHGS 208
Db 294 LSSIKAYLIHYSQMLIYPYSYDYKLPENNAELNNLAKAAVKEL-ATLYGTYKYTGPGA 352
Qy 209 ETLYLAPGGDDWIYDLGIKYSFT 232
Db 353 TTYPAAGGSDWAYDQGIKYSFT 376

Search completed: October 28, 2004, 20:05:52
Job time : 57.2881 secs
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Db 419 TTTATACTGAGGCATCTGATATGCTTACAAAATCCACATGGATCTCTCATTTGAG 478  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaile 60  
Db 479 AAGTACCCTACTATGTTTAAAGGTTTCTGAAAAGAACCAAGCAGCCAAAATGCCATA 538  
Qy 61 TrpLeuAspCysGlyIleHisAlaArgGluTrpLeuSerProAlaPheCysLeuTrpPhe 80  
Db 539 TGGATTGACTGTGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTGTGGTTC 598  
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100  
Db 599 ATAGCCATAATCAATGTGGAGAAACCGTTCTTTCTATGCGAACATCATTTGATC 658  
Qy 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120  
Db 659 GGAACAGACCTGATAGGAACCTTTCTTCCAAACACTGGTGTGAGGAAGTGCATCAGT 718  
Qy 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140  
Db 719 TCCTCATGCTCGAAACCTACTGTGGAATTTATCTGATCAGAACCCAGAAAGTGAAGCA 778  
Qy 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160  
Db 779 GTGGCTAGTTCTTGAGAGAAATATCAACAGATTAAGCATATCATCAGATGCATCA 838  
Qy 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180  
Db 839 TACTCCAGCATATAGTGTTCATATTTCCATATTTATCAGCAAGTAAAGCAAGACCATGAG 898  
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200  
Db 899 GAACGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAATTTAGTAAATAATAC 958  
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAsp 220  
Db 959 AGGTATACATAGCCATGGCTCAGAACTTTATACCTAGCTCTCTGGAGTGGGAGCAT 1018  
Qy 221 TrpLeuTyrAspLeuGlyIleLysTyrSerPhe----- 231  
Db 1019 TGGATCTATGATTGGGCATCAATATTCGTTTACAAATTTGAATTCGAGATACGGGCACA 1078  
Qy 232 -----ThrSerAsnProValGluLysLeuLeuProLeu 243  
Db 1079 TACGATTTCTGTCGGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138  
Qy 243 uSerLeuLys 246  
Db 1139 GTCTCTAAA 1148

## RESULT 2

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PUBLICATION INFORMATION:  
AUTHORS: Eaton, Dan L.  
AUTHORS: Malloy, Beth E.  
AUTHORS: Tsai, Siao P  
AUTHORS: Henzel, William  
AUTHORS: Drayna, Dennis  
TITLE: Isolation, Molecular Cloning, and Partial  
TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
JOURNAL: J. Biol. Chem.  
VOLUME: 266  
ISSUE: 32  
PAGES: 21833-21838  
DATE: No. 5985562 15-1991  
US-08-869-057-1

## Alignment Scores:

Pred. No.: 4,21e-154 Length: 1272  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 2 Gaps: 2

US-09-980-881A-4 (1-246) x US-08-869-057-1 (1-1272)

Qy 1 AlaSerAlaSerTyrTyrGluInTyrH::sSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 343 GCCTCCCGCATCGTACTATGAACAGTATCATCTCAATAATGAAATCTATTCTTGATAGAA 402  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 403 TTTATACTGAGAGGCATCTGATATGCTTACAAAAATCCATTTGGATCTCTCATTTGAG 462  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaile 60  
Db 463 AAGTACCCTACTATGTTTAAAGGTTTCTGAAAAGAACCAAGCAGCCAAAATGCCATA 522  
Qy 61 TrpLeuAspCysGlyIleHisAlaArgGluTrpLeuSerProAlaPheCysLeuTrpPhe 80  
Db 523 TGGATTGACTGTGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTGTGGTTC 582  
Qy 81 IleGlyHis----- 83  
Db 583 ATAGCCATATACTCAATTCTATGGGCAATATACCAATCTCTGAGGCTT 642  
Qy 83 ----- 83  
Db 643 GTGATTTCTATGTTATGCGCGTGGTTAATGTGGCGTTATGACTACTCATGGAAGAAAG 702  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 703 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATCGCAACCAATCATTTGATCGAACAGAC 762  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123

Db 763 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 822  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 823 TCGGAACCTTACTGTGACCTTTATCTGAGTCAGAACAGAGTGAAGGAGGTGGCTAGT 882  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 883 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTTCATCTCCAG 942  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 943 CATATAGTGTTCATATTCCTATACACAGATTAAGCAAGTAAAGCAAGACCATGAGAACTGTCT 1002  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 1062  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPheTyr 223  
Db 1063 CATGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGGATCTAT 1122  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1123 GATTGGGCATCAAAATATTCGTTTACAAATTGAACTTCGAGATACGGGCACATACGGATTC 1182  
Qy 232 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLy 246  
Db 1183 TTGCTGCGGAGCGTTTACATCAACCCCTGTAGAGAAAGCTTTTGGCCGTGCTCTTAA 1242  
Qy 246 s 246  
Db 1243 A 1243

## RESULT 3

US-07-649-591B-2  
; Sequence 2, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161 Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E. 28,616  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: NUCLEIC ACID

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: hybridization probe  
; LOCATION: 133 to 178  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: potential clip site  
; LOCATION: 380 to 382  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: signal sequence  
; LOCATION: 41 to 106  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; US-07-649-591B-2

Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-4 (1-246) x US-07-649-591B-2 (1-1749)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheGlu 20  
Db 383 GCCTCGGCATCGTACTATGAAACAGTATCACTCAATAATGAAATCTATTCTTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProaspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 443 TTTTATAACTGAGAGGCATCTGATATGCTTTACAAAATCCACATTTGGATCCTCATTTGAG 502  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCCACTCTATGTTTAAAGTTTCTGGAAGAAGACAAACAGCCAAATGCCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheIleSerProAlaPheCysLeuTyrPhe 80  
Db 563 TGGATTGACTGTGGAATCCATGCCAGAAATGATCTCTCTGCTTTCTGCTTTGTTGTTTC 622  
Qy 81 IleGlyHis----- 83  
Db 623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTTCTATGTTATGCGGTGGTTAATGTGACGGTTATGACTACTCATGMAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTTGTCATCGGAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTCCTTCCAAACACTGGTGTGAGAAAGGTGCATCCAGTTCCTCATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 863 TCGGAACCTTACTGTGGACTTTTATCTGAGTCAGAACCCAGACAGAGTGAAGCAGGTGGTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTTCATCTCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTTCATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAAGTGTCT 1042

Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTCGGTCTATTGAGAAACCTAGTAAATAATACAGGTATACA 1102  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyr 223  
Db 1103 CATGCCATGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTAT 1162  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1163 GATTGGGCATCAAAATATTCTGTTTACAATTGAACTTCGAGATACGGGCACATACGGATTTC 1222  
Qy 232 -----ThrSerAnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1223 TTGCTGCGGAGCGGTATACATCAAAACCCACCTGTAGAGAAGCTTTGGCGGCTGTCTCTAAA 1282  
Qy 246 s 246  
Db 1283 A 1283  
RESULT 4  
US-08-277-540-2  
; Sequence 2, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/POCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-277-540-2

Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0

Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)  
Qy 1 AlaserAlaserTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 20  
Db 383 GCCTCCCGCATCGTACTATGAACAGTATCTCTCACTAATAAGAAATCTATTTCTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 443 TTTATAACTGAGAGGCATCTGATATGCTTTACAAAAATCCACATTGGATCTCTATTGAG 502  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCCTCTATGTTTAAAGGTTTCTGGAAGAACAAACAGCAACAAATGCCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPhe 80  
Db 563 TGGATTGACTGTGGATCCCATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTC 622  
Qy 81 IleGlyHis----- 83  
Db 623 ATAGGCCATATAACTCAATTCTATGGGATTAATAGGGCAATATACCAATCTCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTCTCTATGTTATGCCGGTGTGTTTAATGTGGACGGTTTATGACTACTCATCGAAAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTCATCGGACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTCCTCCAAACACTCGTGTGAGGAAGGTGCATCCAGTTCTCATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 863 TCGAAACCTTACTGTGGACTTTATCTCTGTGTCAGAACCCAGAGTGAAGGCGAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTTCTGAGAAAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 983 CATATAGTGTTCATATTCTTATACACAGTAAGTAAAGAAAGAACCACTAGTAAACTGTCT 1042  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTCGGTCTATTGAGAAAACTAGTAAAAATACCAAGTATACA 1102  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyr 223  
Db 1103 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTAT 1162  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1163 GATTGGGCATCAAAATATTCTGTTTACAATTCGAGATACGGGCACATACGGATTTC 1222  
Qy 232 -----ThrSerAnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1223 TTGCTGCGGAGCGGTATACATCAAAACCCACCTGTAGAGAAGCTTTGGCGGCTGTCTCTAAA 1282  
Qy 246 s 246  
Db 1283 A 1283  
RESULT 5  
US-08-430-787A-2  
; Sequence 2, Application US/08430787A

Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994

APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91

ATTORNEY/AGENT INFORMATION:  
NAME: Hasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-430-787A-2

Alignment Scores:  
Pred. No.: 7.12e-154 Length: 1749  
Score: 1272.00 Matches: 246

Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20  
Db 383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATTCTGGATAGAA 442

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 443 TTTATACTGAGAGGCATCTGATATCTTACAAAAATCCACATTTGGATCTCATTTGAG 502

Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCACCTCTATGTTTAAAGTTTCTGGAAAAAGACACAGCCAAAATGCCATA 562

Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 563 TGGATTGACTGTGGAATCCATCCAGAGATGGATCTCTCTCTCTCTCTCTCTCTCTCTCT 622

Qy 81 IleGlyHis----- 83  
Db 623 ATAGGCCATATACTCAATTTCTATGGGATAATAGGCAATATACCANTCTCCTGAGGCTT 682

Qy 83 ----- 83  
Db 683 GTGGATTCTATGTTATGTCGGTGTGTTAATGTGACGGTTTACTACTACTCATGAAAAAG 742

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACCAATCATTCATCGGACAGAC 802

Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123  
Db 803 CTGATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 862

Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 863 TCGGAAACCTTACTGTGGACTTTATCTGAGTCAGAACCAAGTGAAGGCAGTGGCTAGT 922

Qy 144 PheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCTTGAGAGAAATATCAACAGATTTAAAGCATATACATCAGCATTCATCTACTCCAG 982

Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGCAATGAGGAAGTGTCT 1042

Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTGCTGCTATTGAGAAAACTAGTAAAAATACCAGTATACA 1102

Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
Db 1103 CATGGCCATGGCTCAGAAACCTTTATACCTAGCTCTGGAGGTGGGACGATTTGATCTAT 1162

Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1163 GATTGGGCATCAAAATATTCGTTTACAATTCGAGATACGGGCACATACGGATTC 1222

Qy 232 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeu 246  
Db 1223 TTGCTGCGGAGGCTTATACATCAAAACCCACCTGTAGAGAGCTTTTGGCGCTGCTCTAAA 1282

Qy 246 s 246  
Db 1283 A 1283

RESULT 6  
US-08-782-760-5  
Sequence 5, Application US/08782760  
Patent No. 5948668  
GENERAL INFORMATION:  
APPLICANT: Hartman, Jacob  
APPLICANT: Fulga, Netta  
APPLICANT: Mendelovitch, Simona  
APPLICANT: Gorecki, Marian  
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
TITLE OF INVENTION: CARBOXYPEPTIDASE B  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
;
US-08-782-760-5

Alignment Scores:
Pred. No.: 8,48e-69 Length: 927
Score: 610.00 Matches: 126
Percent Similarity: 60.50% Conservative: 44
Best Local Similarity: 44.84% Mismatches: 71
Query Match: 45.59% Indels: 41
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-782-760-5 (1-927)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluLeuTyrSerTrpIleGlu 20
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GCAAGTGACACAGCTACCAACAGTACCAACCACTGGGAACGATTGAGCGCTGGATTCAA 60
Qy 21 PhelleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 CAAGTTGCCACTGATTAATCCAGACCTGTCTACTCAGACGCTCATTTGGAAACCAATTGAA 120
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 GGACGTACATGATGTCCTCAAGATT---GGTAAACTAGACCCGGAATAAGCCTGCCATC 177
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 TTCATCATGTTGGTTTCCATCAAGAGAGTGGATTCTCTCGCATTCGTCAAGTGGTTT 237
Qy 81 Ile----- 81
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
238 GTGAGAGAGGCTGTCGTTACCTATAATCAAGAGATCCACATGAAACAGCTTCTAGATGAA 297
Qy 82 -----GlyHis----- 83
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 CTGGATTTCATGTTCTGCTGTCACCATGATGCTATGCTACACCTGGACTAAG 357
Qy 84 AnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
358 GACAGAAATGTGGAGAAAAACCGCTCTACTATGCTGGAAGTTCCTGCTGGGTGTAGAC 417
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 CCCAACGGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCGCGAGCTCCCTGC 474
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
475 TCTGAACACTTACTGTGGACCCAGAGCTCGAAAAAGAGACAAAGGCCCTGGCAGAT 534
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
;
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
;
PCT-US96-00995-5

Alignment Scores:
Pred. No.: 8,48e-69 Length: 927
Score: 610.00 Matches: 126
Percent Similarity: 60.50% Conservative: 44
Best Local Similarity: 44.84% Mismatches: 71
Query Match: 45.59% Indels: 41
DB: 2 Gaps: 5

144 PheLeuArgArgAsnIleAenGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
535 TTCATCGGCAACACTCTCCACCATCAAGGCTACTCTGACCATCCACTACTACTACAG 594
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
595 ATGATGCTCTACCTTACTCTATGACTTCAAACTGCTGAGAACTATGAGGAATTGAAT 654
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
655 GCCTGTGTGAAGGTGGCAAGAGCTT---GCCACTCTGCATGCCACCAAGTACACA 711
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 TATGGCCGAGGAGCTACAACTATTCCTTCCTGCTGGGGGATCTGACGACTGGTCTTAT 771
Qy 224 AspLeuGlyIleLysTyrSerPheThrSurAsnProProValGluLysLeuLeuProLeu 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
772 GATCAGGGAATCAATATTCCTTACTCTGAACTCCGGGATACAGGCTTCTTTGGCTT 830
Qy 244 Ser 244
Db |||||
831 TCT 833

RESULT 7
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
;
PCT-US96-00995-5

Alignment Scores:
Pred. No.: 8,48e-69 Length: 927
Score: 610.00 Matches: 126
```



Percent Similarity: 60.50% Conservatives: 44  
Best Local Similarity: 44.84% Mismatches: 71  
Query Match: 45.59% Indels: 41  
DB: 5 Gaps: 5

US-09-980-881A-4 (1-246) x PCT-US96-00995-5 (1-927)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluIleTyrSerTrpIleGlu 20  
Db 1 GCAAGTGACACAGCTACACCAAGTACAAACATGGGAACGATTGAGGCGTGATCA 60  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 61 CAAGTTGCCACTGATAATCCAGACTTGTCTACTCAGACGCTCATTTGGAACACATTTGAA 120  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIle 60  
Db 121 GGAGTAACTATGATCTCAAGATT---GGTAAACTAGCCGAATAGCCCTGCCATC 177  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 178 TTCATCGATTGTGGTTTCCATGCAAGAGAGTGGATTCTCTCGCATCTGTCAGTGGTTT 237  
Qy 81 Ile----- 81  
Db 238 GTGAGAGAGGCTGCTCGTACCTATAATCAAGAGATCCACATGAACACGTTCTAGATGAA 297  
Qy 82 -----GlyHis----- 83  
Db 298 CTGATTTCTATGTTCTGCTGTGGTCAACATGATGGCTATGTCTACACCTGAGCTAAG 357  
Qy 84 AenArgMetTrpArgLysAenArgSerPheTyrAlaAenAenHisCysIleGlyThrAsp 103  
Db 358 GACAGATGTGGAGAAAACCGCTCTACTATGCTGGAAGTCTCTGTTGGGTGTAGAC 417  
Qy 104 LeuAenArgAenPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 418 CCCAACAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGAGCTTCTCGAGTCCCTGC 474  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 475 TCTGAACCTTACTGTGGACACGCCCGCAGAGTCTGAAAAGAGACAAAGGCCCTGGCAGAT 534  
Qy 144 PheLeuArgArgAenIleAenGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 535 TTCAATCCGCAACACCTCCACCATCAAGGCTTACCTGACCATCCACTCATCTACAG 594  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 595 ATGATGCTCTACCTCTACTCTATGACTACAACTGCTGAGAACTATGAGGAATTGAAT 654  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAenThrArgTyrThr 203  
Db 655 GCCCTGTGAAGGTGGGCAAGAGCTT---GCCACTTGCATGCGCAACAGTACACA 711  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
Db 712 TATGCCCGAGAGCTACACAACTATCTCTGCTGGGGATCTGACGACTGCTTAT 771  
Qy 224 AspLeuGlyIleLysTyrSerPheThrSerAenProProValGluLysLeuLeuProLeu 243  
Db 772 GATCAGGGAATCAATATATCTTTTACCTTTTGAACCT---CCGGGATACAGGCTTCTTTGGCTT 830  
Qy 244 Ser 244  
Db 831 TCT 833

RESULT 8  
US-08-696-139-3  
; Sequence 3, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.

APPLICANT: Greenen, David P.  
APPLICANT: Hershberger, Charles L.  
APPLICANT: Larson, Jeffrey L.  
APPLICANT: Sterner, Jane L.  
APPLICANT: Zhang, Haichao  
TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696,139  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,258  
FILING DATE: 16-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-8681  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..921  
US-08-696-139-3

Alignment Scores:  
Pred. No.: 3,48e-65 Length: 921  
Score: 582.00 Matches: 117  
Percent Similarity: 59.47% Conservative: 40  
Best Local Similarity: 44.32% Mismatches: 67  
Query Match: 43.50% Indels: 40  
DB: 1 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-696-139-3 (1-921)

Qy 6 TyrGluGlnTyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArg 25  
Db 16 TATGAGAGTACAACTCTCTCGCAGCATCGGAAACGATCGAGCTTGGACTAAGCAAGTCACCACTGAA 75  
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45  
Db 76 AATCCAGACCTCATCTCTCGCAGCATCGGAACTACATATTTTAGGAACAATATATAC 135  
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGly 65  
Db 136 CTCCTCAAGGTT---GCCAAACCTGGACCAAAATGAAGCTGCCATTTTCATGAGACTGTGT 192  
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81  
Db 193 TTCCATGCCAGAGAAATGGATTTCCCATGCAATTTTGCAGTGGTTTGTGAGAGAGGCTGTT 252  
Qy 81 ----- 81

Db 253 CTCACCTATGATATGAGAGTCACATGACAGAAATTCCTCAACAGCTAGACTTTATGTC 312  
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88  
Db 313 TTGCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGACCGAATGTGGAGA 372  
Qy 89 LysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108  
Db 373 AAGACCCGCTCTACCAATGCTGGAACCTACCTGCAATTTGGCAGACACCCCAACAGAAATTTT 432  
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerCysSerGluThrTyCys 128  
Db 433 ---GATGCTGGTGTGTCACAACTGGAGCCCTCTACAGACCCCTGGATGAGACTTACTGT 489  
Qy 129 GlyLeuTyProGluSerGluProGluValLysAlaValAlaLaserPheLeuArgArgAsn 148  
Db 490 GGATCTGTCGAGAGTCTGMAAAGAGACCAAGGCCCTGGCTGATTTATACGCAACAC 549  
Qy 149 IleAsnGlnIleLysAlaTyTrpIleSerMetHisSerTyTrpSerGlnHisIleValPhePro 168  
Db 550 CTCCTCTCCATCAAGACATAGCTACGATCCACTCATCTACATGATGATGATGATGATGAT 609  
Qy 169 TyrSerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188  
Db 610 TATTCCTATGATTAACAACTCCCGAGAACAACTGCTGAGTTGAATAAATGCTGGCTAAGGCT 669  
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyThrHisGlyHisGlySer 208  
Db 670 GCGGTGAAGAACTT---GCTACACTGTATGGCACAAGTACATACATAGCCAGGAGCT 726  
Qy 209 GluThrLeuTyLeuAlaProGlyGlyGlyAspTrpIleTyAspLeuGlyIleLys 228  
Db 727 ACAACAATCTATCTGCTGCTGGGGCTCTGATGACTGGGCTTATGACCAAGAAATCAAA 786  
Qy 229 TyrSerPheThr 232  
Db 787 TATTCCTTCAAC 798

## RESULT 9

US-08-696-139-1  
; Sequence 1, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hersberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:

; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1215 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1215  
US-08-696-139-1  
Alignment Scores:  
Pred. No.: 5,49e-65 Length: 1215  
Score: 582.00 Matches: 117  
Percent Similarity: 59.47% Conservative: 40  
Best Local Similarity: 44.32% Mismatches: 67  
Query Match: 43.50% Indels: 40  
DB: 1 Gaps: 5  
US-09-980-881A-4 (1-246) x US-08-696-139-1 (1-1215)  
Qy 6 TyrGluGlnTyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArg 25  
Db 310 TATGAGAAGTACACAACTGGGAAACGACGAGCTTGGACTAAGCAAGTCACCAAGTAA 369  
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTy 45  
Db 370 AATCCAGACCTCATCTCTCGACAGCCACCGGAACACTACATTTTATAGGAAACATATATAC 429  
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65  
Db 430 CTCCTCAAGGTT---GGCAACCTGGACAAATAAGCCTGCCATTTTCATGGAGCTGGT 486  
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81  
Db 487 TTCCATGCCAGAGATGATTTCCCATGCAATTTTGCAGGCTGTTTGTGAGAGAGGCTGTT 546  
Qy 81 -----GlyHis-----AsnArgMetTrpArg 88  
Db 547 CTCACCTATGATATGAGAGTACATGATGAGATTCCTCAACAGCTAGACTTTTATGTC 606  
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88  
Db 607 TTGCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGACCGAATGTGGAGA 666  
Qy 89 LysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108  
Db 667 AAGACCCGCTCTACCAATGCTGGAACTAATCTGCAATTTGGCAGACACCCCAACAGAAATTT 726  
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyCys 128  
Db 727 ---GATGCTGGTGTGTCACAACTGGAGCTCTACAGACCCCTGGATGAGACTTACTGT 783  
Qy 129 GlyLeuTyProGluSerGluProGluValLysAlaValAlaLaserPheLeuArgArgAsn 148  
Db 784 GGATCTGTCGAGAGTCTGMAAAGAGACCAAGGCCCTGGCTGATTTATACGCAACAC 843  
Qy 149 IleAsnGlnIleLysAlaTyTrpIleSerMetHisSerTyTrpSerGlnHisIleValPhePro 168  
Db 844 CTCCTCTCCATCAAGACATAGCTACGATCCACTCATCTACATGATGATGATGATGATGAT 903  
Qy 169 TyrSerTyThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188  
Db 904 TATTCCTATGATTAACAACTCCCGAGAACAACTGCTGAGTTGAATAAATGCTGGCTAAGGCT 963  
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyThrHisGlyHisGlySer 208

Db 964 GCGGTGAAGAAGCTT---GCTACACTGATGGCACCAAGTACACATACGGCCAGAGCT 1020  
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspTyrPheTyrAspLeuGlyIleIys 228  
Db 1021 ACAACAATCTATCTCTGCTGCTGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAA 1080  
Qy 229 TyrSerPheThr 232  
Db 1081 TATTCCTTCAAC 1092

## RESULT 10

US-08-860-882A-67

; Sequence 67, Application US/08860882A

; Patent No. 5985281

; GENERAL INFORMATION:

; APPLICANT: TAYLORSON, CHRISTOPHER JOHN

; APPLICANT: EGGLESTE, HENDRIKUS JOHANNES

; APPLICANT: TARRAGONA-FIOL, ANTONIO

; APPLICANT: RABIN, BRIAN ROBERT

; APPLICANT: BOYLE, FRANCIS THOMAS

; APPLICANT: HENNAM, JOHN FREDERICK

; APPLICANT: BLAKELY, DAVID CHARLES

; APPLICANT: MARSHAM, PETER ROBERT

; APPLICANT: HEATON, DAVID WILLIAM

; APPLICANT: DAVIES, DAVID HUM

; TITLE OF INVENTION: CHEMICAL COMPOUNDS

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON &amp; SUTRO

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/860,882A

; FILING DATE: JUNE 23, 1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: DONALD J. BIRD

; REGISTRATION NUMBER: 25,323

; REFERENCE/DOCKET NUMBER: 9901/238653

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3027

; TELEFAX: (202) 822-0944

; TELEX: 6174627 CUSH

; INFORMATION FOR SEQ ID NO: 67:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 999 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-860-882A-67

## Alignment Scores:

Pred. No.:	3,45e-63	Length:	999
Score:	567.00	Matches:	111
Percent Similarity:	58.36%	Conservative:	46
Best Local Similarity:	41.26%	Mismatches:	72
Query Match:	42.38%	Indels:	40
DB:	2	Gaps:	5

US-09-980-881A-4 (1-246) x US-08-860-882A-67 (1-999)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheGlu 20  
Db 67 GCAACTGCTACTCTTACGAGAAGTACACAAAGTGGGAACGATAGAGGCTTGGACTCAA 126

Qy 21 PheIleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40  
Db 127 CAAGTCCCACTGGAATCCAGCCCTCATCTCTCGAGTGTATCGGAACACACATTTGAG 186  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 187 GGACGCGCTATTTACCTCTCTGAAGTT---GGCAAAGCTGGACAAATAAGCCTGCCATT 243  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPhe 80  
Db 244 TTATGAGACTGTGGTTTCCATGCCAGAGAGTGGATTCTCTCGATTCTGCCAGTGGTTT 303  
Qy 81 Ile----- 81  
Db 304 GTAAGAGAGGCTGTTCTGCTACCTATGGACGTGAGATCCAAGTGACAGAGCTTCTCGACAA 363  
Qy 82 -----GlyHis----- 83  
Db 364 TTAGACTTTTATGTCCTGCTGTGCTCAATATTGATGGCTACATCTACACCTGCACCAAG 423  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCACATCTAGCTAGCTGATCGTGGCAGAC 483  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAAATTTGGAGCTCTCGAAACCCCTGT 540  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 541 GATGAAACTTACTGTGGACCTGCGCAGAGCTCGAAAGGAGACCAAGGCCCTGGCTGAT 600  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 601 TTCAATCGCAACAAACTCTCTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 661 ATGATGATCTACCCCTTACTCATGCTTACAACTCGTGAGAACAAATGCTGAGTTGAAT 720  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 721 GCGCTGGCTAAAGCTACTGTGAAGAACTT---GCCTCACTGCACGCGCACCAAGTACACA 777  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTyrPheTyr 223  
Db 778 TATGGCCCGGAGCTACAAATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 837  
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232  
Db 838 GACCAAGGAATCAGATATTCCTTCACC 864

## RESULT 11

US-09-011-769A-50

; Sequence 50, Application US/09011769A

; Patent No. 643691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; DAVIES, David C.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison &amp; Sutro, LLP

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

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/
/ ZIP: 20005
/
/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: 1.44 Mb disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/09/011.769A
/
/ FILING DATE: 13-Feb-1998
/
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: PCT/GB96/01975
/
/ FILING DATE: 13-AUG-1996
/
/ APPLICATION NUMBER: GB 9612295.7
/
/ FILING DATE: 12-JUN-1996
/
/ APPLICATION NUMBER: GB 9611019.2
/
/ FILING DATE: 25-MAY-1996
/
/ APPLICATION NUMBER: GB 9516810.0
/
/ FILING DATE: 16-AUG-1995
/
/ INFORMATION FOR SEQ ID NO: 50:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 999 base pairs
/
/ TYPE: nucleic acid
/
/ STRANDEDNESS: single
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: other nucleic acid
/
/ FEATURE:
/
/ NAME/KEY: CDS
/
/ LOCATION: 1..987
/
/ FEATURE:
/
/ NAME/KEY: mat_peptide
/
/ LOCATION: 67..987
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 50:
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/ US-09-011-769A-50
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/
/ Alignment Scores:
/
/ Pred. No.: 3.45e-63 Length: 999
/
/ Score: 567.00 Matches: 111
/
/ Percent Similarity: 58.36% Conservative: 46
/
/ Best Local Similarity: 41.26% Mismatches: 72
/
/ Query Match: 42.38% Indels: 40
/
/ DB: 4 Gaps: 5
/
/
/ US-09-980-881A-4 (1-246) x US-09-011-769A-50 (1-999)
/
/ QY 1 AlaSerAlaSerTyTyrgluGlnTyHisSerLeuAsnGluLetyrSertIleGlu 20
/
/ Db 67 GCAACTGGTGCTCTTACGAGAAGTACAAACAAGTGGGAAACGATAGAGGCTTGGACTCAA 126
/
/ QY 21 PheIleThrGluArgHisProAspMetLeuThrlyrIleHisIleGlySerSerPheGlu 40
/
/ Db 127 CAAAGTCGCCACTGAGAANTCCAGCCCTCATCTCTCGCAGTGTATTATCGGAACCAATTGAG 186
/
/ QY 41 LysTyProLeuTyTyValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
/
/ Db 187 GGACGGCGTAITTTACTCTCTGAGGTT---GGCAAGCTGGACAAATAAGCTGCAATT 243
/
/ QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
/
/ Db 244 TTCAATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCTCTGCAATTCGCCAGTGGTTT 303
/
/ QY 81 Ile----- 81
/
/ Db 304 GTAAGAGAGGCTGTTCTGATACCTATGGACGTGAGATCCAAGTCGACAGAGCTTTCGACAAG 363
/
/ QY 82 -----GlyHis----- 83
/
/ Db 364 TTAGACTTTTATGCTCTGCTGTGCTCAATATTGATGGCTACATCTACACCTGACCAAG 423
/
/ QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAsp 103
/
/ Db 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCATCTGATCGATCTAGCTCATTTGGCAGAC 483

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-860-882A-64

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-64 (1-1053)

Qy 1 AlaSerAlaSerTyTyTyGluGluTyHisSerLeuAsnGluIleTySerTrpIleGlu 20
Db 67 GCAACTGGTCACTCTTACGAGAAGTACAAACAAAGTGGGAAACGATAGAGGCTTGACCTCAA 126

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 127 CAAGTCGCCACTGAGAAATCCAGCCCTCATCTCCAGTGTATCGGAACCCACATTGGAG 186

Qy 41 LysTyProLeuTyValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaIle 60
Db 187 GGACGGCGTATTTACCTCTCGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243

Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 244 TTCATGACTGTGGTTCCATGCCAGAGTGGATTTCTCTGCTATCTCGCAGTGGTTT 303

Qy 81 Ile-----GlyHis----- 81
Db 304 GTAAGACGAGGCTGTTCGTACCTACCTGAGCTGAGATCCAAAGTGACAGAGCTTCTCGACAAG 363

Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGTCCTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 103
Db 424 AGCGATTTTGGAGAAAGACTCGCTCCACCATACTGATCTAGCTGCTGCTGCTGCTGCTGCTG 483

Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 484 CCCAACAGAAATTT---GATGCTGTTGGTGTGAAATTTGGAGCTCTCGAAACCCCTGT 540

Qy 124 SerGluThrTyTyCysGlyLeuTyTyProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATGAAACTTACTGTGGACCTGCGCAGAGTCTGAAAGAGGAGACCAAGGCCCTGGCTGAT 600

Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGln 163
Db 601 TTATCCGCAACAACACTCTCTTCATCAGGATATCTGAAATCCACTCGTACTCCCAA 660

Qy 164 HisIleValPheProTyTySerTyTyArgSerLysSerLysAspHisGluGluLeuSer 183
Db 661 ATGATGATCTACCTTACTCATATGCTTACAACTCGTGCAGAACATGCTGAGTTGAAT 720

Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAGAAGACTT---GCCTCACTGACGCGCACCAAGTACACA 777

Qy 204 HisGlyHisGlySerGluThrLeuTyTyLeuAlaProGlyGlyGlyAspTrpIleTy 223
Db 778 TATGGCCCGGAGGCTACAAACAATCTATCTGCTGCTGGGGGCTCTGACGAGCTGGCTTAT 837

Qy 224 AspLeuGlyIleLysTyTySerPheThr 232
Db 838 GACCAAGGAATCAGATATCTCTTACC 864

RESULT 13
US-09-011-769A-46
; Sequence 46, Application US/09011769A
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; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1053 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1047
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..1047
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-011-769A-46

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-46 (1-1053)

Qy 1 AlaSerAlaSerTyTyTyGluGluTyHisSerLeuAsnGluIleTySerTrpIleGlu 20
Db 67 GCAACTGGTCACTCTTACGAGAAGTACAAACAAAGTGGGAAACGATAGAGGCTTGACCTCAA 126

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 127 CAAGTCGCCACTGAGAAATCCAGCCCTCATCTCCAGTGTATCGGAACCCACATTGGAG 186

Qy 41 LysTyProLeuTyValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaIle 60
Db 187 GGACGGCGTATTTACCTCTCGAAGGTT---GGCAAAGCTGGACAAAATAAGCCTGCCATT 243
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Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 244 TTCATGGACTGTGGTTTCCATGCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 303
Qy 81 Ile----- 81
Db 304 GTAAGAGAGGCTGTTGCTACCTATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAAG 363
Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGTCCTGCTGCTCAATATTGCTACATCTACACCTGACCAAG 423
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
Db 424 AGCGGATTTTGGAGAAAGACTCGCTCCACCATATCTGATCTAGCTGCAITGGCAGAC 483
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 484 CCCAACAGAAATTTT---GATGCTGGTTGGTGGATTTGGAGCCTCTCGAAACCCCTGT 540
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATGAACCTTACTGTGACCTGCCGACAGTCTGAAAGGAGACCAAGGCCCTGGCTGAT 600
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 601 TTCATCGCAACAACCTCTCTCCATCAAGGCATATCTGACAAATCCATCTGCTACTCCAA 660
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 661 ATGATGATCTACCTTACTCATATGCTTACAACTCGGTGAGAACATGCTGATTTGAAT 720
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAGAAGCTT---GCCCTACTGCACGGCACCACCAAGTACACA 777
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 223
Db 778 TATGCCCGGAGCTACAAACATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 837
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232
Db 838 GACCAAGGAATCAGATATTCCTTACC 864
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## RESULT 14

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US-08-860-882A-56
Sequence 56, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGLESE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESS: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238613
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1263 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-56
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Alignment Scores:
Pred. No.: 5,08e-63 Length: 1263
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5
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US-09-980-881A-4 (1-246) x US-08-860-882A-56 (1-1263)

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Qy 1 AlaSerAlaSerTyrTyrGluGluTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 325 GCAACAGGACACAGTATGAGAAGTACACAACTGGGAAACGATAGAGGCTTGACCTCAA 384
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 385 CAAGTCGCCACTGAGATCCAGCCCTCACTCTCGCAGTGTATCGAACACCATTTGAG 444
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 445 GGACGCGCTATTACCTCTCTGAAGTT---GGCAAGCTGCACAAATAAGCCTGCCATT 501
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTrpPhe 80
Db 502 TTCATGGACTGTGGTTTCCATGCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 561
Qy 81 Ile----- 81
Db 562 GTAAGAGAGGCTGTTGCTACCTATGGACCTGAGATCCAAAGTGACAGAGCTTCTCGACAAG 621
Qy 82 -----GlyHis----- 83
Db 622 TTAGACTTTTATGCTGCTGCTGCTCAATATTGATGGCTACATCTACACCTGACCAAG 681
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
Db 682 AGCGGATTTTGGAGAAAGACTCGCTCCACCTACTGATCTAGCTGCAITGGCAGAC 741
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 742 CCCAACAGAAATTTT---GATGCTGGTTGGTGGATTTGGAGCCTCTCGAAACCCCTGT 798
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 799 GATGAACCTTACTGTGACCTGCCGACAGTCTGAAAGGAGGACCAAGGCCCTGGCTGAT 858
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 859 TTCATCGCAACAACCTCTCTCCATCAAGGCATATCTGACAAATCCATCTGCTACTCCAA 918
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
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Db 919 ATGATGATCTACCTTACTCATCTATCTGTACAACTCGGTGAGAACAAATGCTGAGTTGAAT 978  
Qy 184 LeuValAlaSerGluAlaValArgAlaValGluLysThrSerLysAsnThrArgTyrThr 203  
Db 979 GCCCTGGTAAAGTACTGTGAAGAAGCTT---GCCCTACTGACCGCACCAAGTACACA 1035  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPheTyr 223  
Db 1036 TATGCCCGGAGCTACAAACAATCTATCTGCTGCTGCGGCTCTGTGACGACTGGGCTTAT 1095  
Qy 224 AspLeuGlyLeuLysTyrSerPheThr 232  
Db 1096 GACCAAGGAATCAGATATTCCTTACC 1122

## RESULT 15

US-09-011-769A-38  
; Sequence 38, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLAYER, Anthony M.  
; BLAKEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011.769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1263 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38

Alignment Scores:  
Pred. No.: 5.08e-63 Length: 1263  
Score: 567.00 Matches: 111  
Percent Similarity: 58.36% Conservative: 46  
Best Local Similarity: 41.26% Mismatches: 72  
Query Match: 42.38% Indels: 40  
DB: 4 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-38 (1-1263)

Qy 1 AlaserAlaserTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTyrPheGlu 20  
Db 325 GCAACGAGGACACAGTTATGAGAAGTACAAACAAGTGGGAAACAGTAGAGGCTTGGACTCAA 384  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 385 CAAGTCGCCACTGAGATCCAGCCCTCATCTCTCGAGTGTATTATCGGAACCAATTTGAG 444  
Qy 41 LysTyrProLeuThrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 445 GGACGGCTATTACCTCTCTGAAGTT---GGCAAGCTGGACAAATAAGACCTGCCATT 501  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPhe 80  
Db 502 TTCATGGACTGTGTTTCCATGCCAGAGAGTGTATCTCTGCATTCTCCAGTGGTTT 561  
Qy 81 Ile----- 81  
Db 562 GTAAGAGAGGCTGTTCGTACTATGGACGTGAGATCCAAGTGCAGAGCTTCTCGACAAG 621  
Qy 82 -----GlyHis----- 83  
Db 622 TTAGACTTTTATGCTGCTGCTCAATATTGATGGCTATCATCTACACTGGACCAAG 681  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 682 AGCCGATTTTGGAGAAAGACTCGCTCCACCATACTGGATCTAGCTGCTATGGCAGAC 741  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123  
Db 742 CCCAACAGAAATTTT---GATGCTGGTGTGTGTAATTTGGAGCCTCTCGAAACCCCTGT 798  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 799 GATGAACCTTACTGTGGACCTCGCGCAGAGCTCTGAAAGAAACCAAGCCCTGGCTGAT 858  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMethHisSerTyrSerGln 163  
Db 859 TTCATCGCAACAAACTCTCTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 918  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
Db 919 ATGATGATCTACCTTACTCATATGCTTACAAACTCGGTGAGAACAAATGCTGAGTTGAAT 978  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 979 GCCTGGCTAAAGCTACTGTGAAGAAGACTT---GCCTCACTGACGGCACCAAGTACACA 1035  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrPheTyr 223  
Db 1036 TATGCCCGGAGCTACACAAATCTATCTGCTGCTGCGGCTCTGTGACGACTGGGCTTAT 1095  
Qy 224 AspLeuGlyLeuLysTyrSerPheThr 232  
Db 1096 GACCAAGGAATCAGATATTCCTTACC 1122

Search completed: October 31, 2004, 04:40:06  
Job time : 78.6631 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 31, 2004, 04:28:49 ; Search time 428.415 Seconds  
(without alignments)  
2944.316 Million cell updates/sec

Title: US-09-980-881A-4

Perfect score: 1338

Sequence: 1 ASASYBYQYHSLNEIYSWIE.....IKYSFTSNPPVEKLLPLSLK 246

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Fgapop 10.0 , Fgapext 0.5

Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 256380928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09980881@cgn 1 1 811 @runat\_28102004\_131644\_12110  
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-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:  
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7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
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9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	1289.5	96.4	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1289.5	96.4	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1272	95.1	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1248.5	93.3	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1248.5	93.3	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1177	88.0	1272	15	US-10-379-836-1	Sequence 1, Appli
7	902	67.4	1400	9	US-09-925-302-24	Sequence 24, Appl
8	902	67.4	1400	10	US-09-925-302-24	Sequence 24, Appl
9	869.5	65.0	1037	16	US-10-115-479-63	Sequence 63, Appl
10	830.5	62.1	1132	16	US-10-115-479-65	Sequence 65, Appl
11	556.5	41.6	1302	17	US-10-477-515-1	Sequence 1, Appli
12	556.5	41.6	1311	13	US-10-200-344-9	Sequence 9, Appli
13	556.5	41.6	1993	15	US-10-274-639-33	Sequence 33, Appl
14	556.5	41.6	1993	16	US-10-333-574-33	Sequence 33, Appl
15	554.5	41.4	1907	18	US-10-757-262-127	Sequence 127, App
16	552	41.3	1254	14	US-10-229-546-3	Sequence 3, Appli
17	552	41.3	1622	14	US-10-229-546-1	Sequence 1, Appli
18	552	41.3	1622	15	US-10-429-803-21	Sequence 21, Appl
19	552	41.3	1622	16	US-10-430-503-12	Sequence 12, Appl
20	552	41.3	1622	16	US-10-262-511-71	Sequence 71, Appl
21	552	41.3	1622	16	US-10-641-643-1020	Sequence 1020, Ap
22	552	41.3	1633	15	US-10-341-434-187	Sequence 187, App
23	552	41.3	1740	14	US-10-116-802-95	Sequence 95, Appl
24	550.5	41.1	1125	9	US-09-888-615-2	Sequence 2, Appli
25	550.5	41.1	1332	15	US-10-176-306-75	Sequence 75, Appl
26	550.5	41.1	1603	15	US-10-176-306-73	Sequence 73, Appl
27	549	41.0	1870	9	US-09-910-059-112	Sequence 112, App
28	549	41.0	1870	17	US-10-608-710-3	Sequence 3, Appli
29	549	41.0	2154	9	US-09-910-059-124	Sequence 124, App
30	547.5	40.9	1332	9	US-09-954-456-1141	Sequence 1141, Ap
31	543.5	40.6	1826	15	US-10-252-157-453	Sequence 453, App
32	533.5	39.9	991	16	US-10-383-201-93	Sequence 93, Appl
33	525.5	39.3	12128	13	US-10-200-344-13	Sequence 13, Appl
34	523.5	39.1	1295	17	US-10-363-829-148	Sequence 148, App
35	492	36.8	1200	14	US-10-200-910-7	Sequence 7, Appli
36	492	36.8	1200	18	US-10-843-130-7	Sequence 7, Appli
37	471.5	35.2	1050	13	US-10-200-344-11	Sequence 11, Appl
38	465.5	34.8	1254	9	US-09-925-297-58	Sequence 58, Appl
39	465.5	34.8	1260	15	US-10-345-680-66	Sequence 66, Appl
40	465.5	34.8	1260	16	US-10-236-417-16	Sequence 16, Appl
41	465.5	34.8	1279	16	US-10-236-417-217	Sequence 217, App
42	465.5	34.8	1290	16	US-10-236-417-219	Sequence 219, App
43	465.5	34.8	1311	14	US-10-200-910-5	Sequence 5, Appli
44	465.5	34.8	1311	16	US-10-257-174-15	Sequence 15, Appl
45	465.5	34.8	1311	17	US-10-451-821-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813, 133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1  
Alignment Scores:

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Pred. No.: 1.39e-159 Length: 1625
Score: 1289.50 Matches: 244
Percent Similarity: 92.42% Conservative: 0
Best Local Similarity: 92.42% Mismatches: 2
Query Match: 96.38% Indels: 18
DB: 9 Gaps: 1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGTATCACTCAATAATGAATCTATTCTTGGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCACCTCTATGTTTAAAGGTTTTCGAAAAAGAACAGCAGCAAAAATGCCATA 538
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheTyrHisSerProAlaPheCysLeuTrpPhe 80
Db 539 TGGATTGACTGTGGAATCCATGAGAGTATGATCTCTCTGCTTCTGCTTGTGGTTC 598
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 599 ATAGGCCATAATCGAATGTGAGAAAGATCGTCTTCTTCTATGCGAACAAATCATTCATCA 658
Qy 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
Db 659 GGAACAGACCTGAAATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAG 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACTGCTCTAGTAGCCAGTGAAGCAGTTCGGTCTATTGAGAAAAATAGTAAAAATACC 958
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAsp 220
Db 959 AGGTATACACATGCGCATGCGTCAAAACCTTATACCTAGCTCTCTGGAGGTGGGGAGCAT 1018
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 1019 TGGATCTATGATTGGGCATCAAAATATTCGTTTACAATTGAACCTTCGAGATACGGGCACA 1078
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 1079 TACGATTCTTGTGCGGAGCGTTACATCAACCCACCTCTAGAGAAGCTTTTGGCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASES PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores: 1.39e-159 Length: 1625
Pred. No.: 1289.50 Matches: 244
Score: 1289.50 Conservative: 0
Percent Similarity: 92.42% Mismatches: 2
Best Local Similarity: 92.42% Indels: 18
Query Match: 96.38%
DB: 14 Gaps: 1

US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGTATCACTCAATAATGAATCTATTCTTGGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCACCTCTATGTTTAAAGGTTTTCGAAAAAGAACAGCAGCAAAAATGCCATA 538
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheTyrHisSerProAlaPheCysLeuTrpPhe 80
Db 539 TGGATTGACTGTGGAATCCATGAGAGTATGATCTCTCTGCTTCTGCTTGTGGTTC 598
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 599 ATAGGCCATAATCGAATGTGAGAAAGATCGTCTTCTTCTATGCGAACAAATCATTCATCA 658
Qy 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
Db 659 GGAACAGACCTGAAATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAG 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACTGCTCTAGTAGCCAGTGAAGCAGTTCGGTCTATTGAGAAAAATAGTAAAAATACC 958
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAsp 220
Db 959 AGGTATACACATGCGCATGCGTCAAAACCTTATACCTAGCTCTCTGGAGGTGGGGAGCAT 1018
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 1019 TGGATCTATGATTGGGCATCAAAATATTCGTTTACAATTGAACCTTCGAGATACGGGCACA 1078
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 1079 TACGATTCTTGTGCGGAGCGTTACATCAACCCACCTCTAGAGAAGCTTTTGGCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASES PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
```

Db 1079 TACGATTCTTGTCCGCGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138  
Qy 243 userLeuLys 246  
Db 1139 GTCTCTAAAA 1148  
RESULT 3  
US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vocklev, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396  
Alignment Scores:  
Pred. No.: 3,17e-157 Length: 1728  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 9 Gaps: 2  
US-09-880-881A-4 (1-246) x US-09-880-107-2396 (1-1728)  
Qy 1 AlasSerAlaSerTyrGluGlnTyrHisSerLeuAenGluLeuTyrSerTrpIleGlu 20  
Db 362 GCCTCCGCGATCGTACTATGACAGATATCACTCACTAAATGAAATCTATTCTTGGATAGAA 421  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 422 TTTATACTGAGAGGCATCCTGATATGCTTACAAAATCCACATTTGGATCTCATTTGAG 481  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIle 60  
Db 482 AAGTACCACCTCTATGTTTAAAGGTTTCTGGAAGAAACAAACAGCCAAAATGCCATA 541  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 542 TGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCTGCTTTTCTGCTTGTGGTTC 601  
Qy 81 IleGlyHis-----83  
Db 602 ATAGCCATATACTCAATCTTATGGGTAATAGGGCAATATACCAATCTCTCAGGCTT 661  
Qy 83 -----83  
Db 662 GTGGATTCTATGTTATGCGGTGGTTAATGTGGACGGTTATGACTACTCATCGAAGAAAG 721  
Qy 84 AsnArgMetTrpArgLysAenArgSerPheTyrAlaAenHisCysIleGlyThrAsp 103  
Db 722 AATCGAATGTGGAAAGAACCGGTTCTTCTATCGAACAATCATATTCATCGGAACAGAC 781  
Qy 104 LeuAenArgAenPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123

Db 782 CTCAATAGGAACCTTGTCTTCCAAACACATGCTGTGTGAGGAAGGTGCATCCAGTCTCTCATGC 841  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 842 TCGGAACCTTACTGTGTGACTTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGAGTGGCTAGT 901  
Qy 144 PheLeuArgArgAenIleAenGlnIleLysAlaTyrIleSerMethHisSerTyrSerGln 163  
Db 902 TTCTTGAGAAGAAATATCAACCAAGATTAAAGCATACATCAGCATGCATTCATCTACTCCAG 961  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 962 CATATAGTGTTCATATTCCTATACACGAAGTAAAAAGCAAGACCATGAGGAACCTGTCT 1021  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAenThrArgTyrThr 203  
Db 1022 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACCTAGTAAAAATACCAAGTATACA 1081  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyGlyAspTrpIleTyr 223  
Db 1082 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGGATCTAT 1141  
Qy 224 AspLeuGlyIleLysTyrSerPhe-----231  
Db 1142 GATTGGGCATCAATATATTCGTTTACAATTGAACCTTCGAGATACGGGCACATACGGATTC 1201  
Qy 232 -----ThrSerAenProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1202 TTCTGCCGCGAGCGTTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1261  
Qy 246 s 246  
Db 1262 A 1262  
RESULT 4  
US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zernhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkete, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03

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; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.: 2 71e-154 Length: 1344
Score: 1248.50 Matches: 244
Percent Similarity: 79.74% Conservative: 0
Best Local Similarity: 79.74% Mismatches: 2
Query Match: 93.31% Indels: 60
DB: 16 Gaps: 3

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluileTyrSerTrpIleGlu 20
Db 373 GCCTCCGATCGTACTATGAACAGATATCACTCACTAAATGAATCAATCTTTGGATAGAA 432
Qy 21 PheIleThrGluArgHisProAspMetLeuThrIlylsIleHisIleGlySerSerPheGlu 40
Db 433 TTTTAACGTAGAGGCATCCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAG 492
Qy 41 LysTyrProLeuTyrValIleuLys-----ValSerGlyLysGluGlnThr 55
Db 493 AAGTACCACCTCTATGTTTTAAAGGGTTCTTTGAGCGGGTTCTGGAAAAGAACAGCA 552
Qy 56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
Db 553 GCCAAAAATGCCATATGATTTGACTGTGGAAATCCATGCCAGAGAAATGATCTCTCCTGCT 612
Qy 76 PheCysLeuTrpPheIleGlyHis----- 83
Db 613 TTCTGCTGTGGTTTCATAGGCCATATACTCAATTTCTATGGGATAAATAGGCAATATACC 672
Qy 83 ----- 83
Db 673 AATCTCTGAGCGTTGTGGATTTCTATGTTATGCGGGTGGTTAATGTGGATGGTTATGAC 732
Qy 84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
Db 733 TACTCATGGAAAAAGAAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCAT 792
Qy 99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerIysHisTrpCysGluGluGlyAla 118
Db 793 TGCATCGGAACAGACCTGAATAGGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCA 852
Qy 119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
Db -----

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Db 853 TCAGTTCTCATGCTCGGAAACCTACTTGTGGACTTTTATCTCTGAGTCAGAACCAAGAGTG 912
Qy 139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
Db 913 AAGGCAGTGGCTAGTTCTTTGAGAAGAAATATCAACCCAGATTAAAGCATACATCAGCATG 972
Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
Db 973 CATTCACTACCTCCAGCATATAGTGTTCATATATCTTATACAGAAATAAAGCAAGAC 1032
Qy 179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
Db 1033 CATGAGGAACCTGCTCTTAGTAGCCAGTGAAGCAGTTCTGCTATTGAGAAAATTAGTAAA 1092
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrIleuAlaProGlyGlyGly 218
Db 1093 AATACCAGGTATACACATGGCATGGCTUAGAAAACCTTATACCTAGCTCCTCGGAGGTGGG 1152
Qy 219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 1153 GACGATTGGATCTATGATTTTGGGCATCATATATTCGTTTACAATTGAACCTTCGAGATACG 1212
Qy 232 -----ThrSerAsnProProValGluLysLeuLe 241
Db 1213 GGCACATACGGATCTTTGCTGCCGGAGCATTACATCAAAACCCACCTGTAGAGAAGCTTTT 1272
Qy 241 uProLeuSerLeuLys 246
Db 1273 GCCGCTGCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; TITLE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934

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;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 67  
;; LENGTH: 1743  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (20)..(1304)  
US-10-115-479-67

Alignment Scores:  
Pred. No.: 4.12e-154 Length: 1743  
Score: 1248.50 Matches: 244  
Percent Similarity: 79.74% Conservative: 0  
Best Local Similarity: 79.74% Mismatches: 2  
Query Match: 93.31% Indels: 60  
DB: 16 Gaps: 3

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluLyleTyrSerTrpIleGlu 20  
Db 362 GCCTCCGATCGTACTATGACAGTATCACTCACTAAATGAAATCTATCTTGATAGAA 421  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 422 TTTATACCTGAGGCGATCTGATATGCTTACAAAATCCACATGGATCTCTCTGCT 481  
Qy 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55  
Db 482 AAGTACCACCTCTATGTTTAAAGGGTTCTTTGAGCAGCGTTCTCGGAAAGAACAGCA 541  
Qy 56 AlaLysAenAlaIleTrpIleAspCysGlyLleHisAlaArgGluTrpIleSerProAla 75  
Db 542 GCCAAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAAATGGATCTCTCTGCT 601  
Qy 76 PheCysLeuTyrPheIleGlyHis----- 83  
Db 602 TTTGCTTGTTGTTATAGGCCATATACTCAATTCATGGGATAATAGGCAATATACC 661  
Qy 83 ----- 83  
Db 662 AATCTCTGAGGCTTGATTTCTATGTTATGCCAGTGGTTAATGTGGATTATGAC 721  
Qy 84 -----AsnArgMetTrpArgLysAenArgSerPheTyrAlaAenAsnHis 98  
Db 722 TACTCATGGAAAAAGAAATCGAAATGGGAAAGAACCGTTCTTTCTATGCGAAACAATCAT 781  
Qy 99 CysIleGlyThrAspLeuAenArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118  
Db 782 TGCATCGGAACAGACCTGGAATAGGAATCTTCTTCCAAACACTGGTGTGAGGAAGGTGCA 841  
Qy 119 SerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138  
Db 842 TCCAGTTCCTCATCTCGGAAACCTACTGTGGACTTTATCTGAGTCAGAACCAAGATG 901  
Qy 139 LysAlaValAlaSerPheLeuArgAsnIleAenGlnIleLysAlaTyrIleSerMet 158  
Db 902 AAGGCAGTGGCTAGTTCTTGGAGAAAGAAATATCAACAGATTAAAGCATACATCAGCATG 961

Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178  
Db 962 CATTCATACTCCAGCATATAGTGTTCATATCTCTATACAGNAGTAAGCAAGAC 1021  
Qy 179 HisGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198  
Db 1022 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATTAGTAA 1081  
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGly 218  
Db 1082 AATACCAAGGTATACACATGCCATGGCTCAGAACCTTATACCTAGTCTCTGAGGTGG 1141  
Qy 219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231  
Db 1142 GACGATTGGATCTATGATTGGGCATCAATATATCGTTTACAAATTGAACTTCGAGATACG 1201  
Qy 232 -----ThrSerAsnProProValGluLysLeuLe 241  
Db 1202 GGCACATACGATTTCTTGCTCGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTT 1261  
Qy 241 uProLeuSerLeuLys 246  
Db 1262 GCGCTGCTCTCTAAAA 1277

# RESULT 6

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; TITLE OF INVENTION: TAFI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

Alignment Scores:  
Pred. No.: 7.14e-145 Length: 1272  
Score: 1177.00 Matches: 228  
Percent Similarity: 78.41% Conservative: 8  
Best Local Similarity: 75.75% Mismatches: 10  
Query Match: 87.97% Indels: 55  
DB: 15 Gaps: 2

US-09-980-881A-4 (1-246) x US-10-379-836-1 (1-1272)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAenGluLyleTyrSerTrpIleGlu 20  
Db 343 GCCTCCGATCGTACTATGACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAA 402  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 403 CTTTAACTGAGAAAGTATCTGATATGCTTACAAAAATCCACATTCGATCTCTCTATGAG 462  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIle 60  
Db 463 AAGCACCCTCTTATGTTTAAAGGTTCTGGAAGAAACAAACAGCCAAAATATGCCATG 522  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80

Db 523 TGGATTGACTGTGGAATCCATGCCAGAAATGGATCTCCCTGCTTTCTGCTTGTGGTTC 582  
Qy 81 IleGlyHis----- 83  
Db 583 ATAGCCATATACTGAATACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCAT 642  
Qy 83 ----- 83  
Db 643 GTGGATTCTTATGTTATGCCAGTGGTTAATGTGGATGTTATGACTACTCATGAGAAAAG 702  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 703 AATCGAATGTGGAGAAAGACCGTCTTCTATGCGAACAATCGTTGCATCGGAACAGAC 762  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 763 CTGAACAGGAACCTTTGCGCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGC 822  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 823 TCAGAAACCTACTGTGGACTTTATCTCGAGTCAGAACCAAGCAAGCGGTGGCTAAT 882  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 883 TTCTTGAGAGAAATATCAACACATTAACATACATACATGATGATTCATCTCCAG 942  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 943 CATATCGTGTTCCTATATCTCTATCTCGAAGCAAAAGCAAGCAAGCAAGCAAGTGTCT 1002  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACCAAGTAAATAATATCAGGTATACA 1062  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
Db 1063 CATGCCCTGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGACCAATGATCTAT 1122  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1123 GATTGGGCATCAATAATTCGTTTACAATTGAACTTCGAGATCGGGCAAAATACGGATTC 1182  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1183 TTGCTGCTGAGCGGTATACATCAAAACCCACTTGTAAAGACGCTTTTGGCGCTGTCTCTAAA 1242  
Qy 246 s 246  
Db 1243 A 1243

## RESULT 7

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c;  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 1.99e-108 Length: 1400  
Score: 902.00 Matches: 181  
Percent Similarity: 76.05% Conservative: 0  
Best Local Similarity: 76.05% Mismatches: 1  
Query Match: 67.41% Indels: 56  
DB: 9 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy 65 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83  
Db 10 GGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCATATA 69  
Qy 83 ----- 83  
Db 70 ACTCAATCTTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTAT 129  
Qy 84 -----AsnArgMetTr 87  
Db 130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACACTACTCATGGAAGAAATCGAATGTG 189  
Qy 87 PArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107  
Db 190 GAGAAAGAACCGTCTTCTTCTATGCGAACATATCATGTCATCGGAACAGACCTGAATAGAA 249  
Qy 107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 127  
Db 250 CTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTA 309  
Qy 127 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147  
Db 310 CTGTGGACTTTATCTCAGTCAGAACCAAGTGAAGGCAAGTGGCTAGTTCTTTGAGAAG 369  
Qy 147 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 167  
Db 370 AAATATCAACGAGATTAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGT 429  
Qy 167 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187  
Db 430 TCCATATTTCTATACAGAAAGTAAAGCAAGCAATGAGAACTGTCTCTAGTAGCCAG 489  
Qy 187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisG 207  
Db 490 TGAAGCAGTTCTGCTATTGAGAAACTGTAAAAATACCAAGGTATACACATGGCCATGG 549  
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyI 227  
Db 550 CTCAGAAACCTTATACCTAGCTCTCGAAGTGGGGACGATTTGGATCTATGATTTGGGCAT 609  
Qy 227 eLysTyrSerPhe----- 231  
Db 610 CAAATATTCGTTTACAATTGAACTTCGAAATACGGGCACATACCGGATTTCTGCTGCCGA 669  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 670 GCGTTACATCAAAACCCACTGTAGAGAAAGCTTTTGGCGCTGTCTCTAAAA 719

## RESULT 8

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 1.99e-108 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservative: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 67.41% Indels: 56
DB: 10 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy 65 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATA 69
Qy 83 ----- 83
Db 70 ACTCAATTCATGGGATAATAGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTAT 129
Qy 84 -----AsnArgMetTr 87
Db 130 GTATGCGCGTGTATATGGATGGTTATGAACACTCTCATCGAAGAAATCGAATGTC 189
Qy 87 pArgLysAsnArgSerPheTyRAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107
Db 190 GAGAAAGAACCGTCTTCTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAATGAA 249
Qy 107 nPheAlaSerIyHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 127
Db 250 CTTTGTCTTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTA 309
Qy 127 rCysGlyLeuTyxProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147
Db 310 CTGTGGACTTTATCTGAGTCAGACAGACCAGAGTGAAGGAGTGGCTAGTTTCTTGAGAAG 369
Qy 147 gAsnIleAsnGlnIleLysAlaTyRlleSerMetHisSerTyxSerGlnHisIleValPh 167
Db 370 AAATATCAACAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGT 429
Qy 167 eProTyxSerTyxThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187
Db 430 TCCATATTCCTATACAGAAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAG 489
Qy 187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyRThrHisGlyHisGl 207
Db 490 TGAAGCAGTTCGTGCTATTGAGAAATACTAGTAAATAACAGGTATACATGCGCCATGG 549
Qy 207 ySerGluThrLeuTyRleuAlaProGlyGlyAspAspTrpIleTyRAspLeuGlyIl 227
Db 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTGGGCAT 609
Qy 227 eLysTyxSerPhe----- 231
Db 610 CAAATATTCGTTTACAAATTCGAACCTCGAGATACGGGCACATACCGAATTCCTTGTCCGGGA 669
Qy 232 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 246
Db 670 GCGTTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 719

RESULT 9

US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malvanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 2.45e-104 Length: 1037
Score: 869.50 Matches: 180
Percent Similarity: 68.18% Conservative: 0
Best Local Similarity: 68.18% Mismatches: 2
Query Match: 64.99% Indels: 82
DB: 16 Gaps: 2

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US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)
Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATCTTGGATAGAA 442
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTGAG 502
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 503 AAGTACCACCTCTATGTTTAAAGGTTTCTGGAAGAGAACAGCAGCAGCAAAAATGCCATA 562
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 563 TGGATTGAC----- 571
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIle 100
Db 571 ----- 571
Qy 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
Db 571 ----- 571
Qy 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
Db 572 -----TGTGGACTTTATCCTGAGTCAGAACCCAGAAAGTGAAGGCA 610
Qy 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
Db 611 GTGGCTAGTTCTTTCAGAGAAGAAATATCAACAGAGATTAAAGCATATCATCAGCATCATCA 670
Qy 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
Db 671 TACTCCAGCATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATGAG 730
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 731 GAACGTCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAATAGTAAAAATACC 790
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAsp 220
Db 791 AGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCCTGGAGGTGGGGACGAT 850
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 851 TGGATCTATGATTGGGCATCAATATTCGTTTACAAATTGAACCTCGAGATACGGGCACA 910
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 911 TACGGATCTTGTGCGGAGCGTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 970
Qy 243 uSerLeuLys 246
Db 971 GTCTCTAAAA 980
RESULT 10
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
```

```
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shmukets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-322 B (Cura 622 Pt)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 65
LENGTH: 1132
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (41)..(1103)
US-10-115-479-65
Alignment Scores:
Pred. No.: 4,07e-99 Length: 1132
Score: 830.50 Matches: 171
Percent Similarity: 55.88% Conservative: 0
Best Local Similarity: 55.88% Mismatches: 1
Query Match: 62.07% Indels: 134
DB: 16 Gaps: 4
US-09-980-881A-4 (1-246) x US-10-115-479-65 (1-1132)
Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATCTTGGATAGAA 442
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTGAG 502
Qy 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55
```





```
; Sequence 9, Application US/10200344
; Publication No. US20020173641A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020173641A1el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.: 9,08e-63 Length: 1311
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 13 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
Db 406 TATGAGTTTATCTCTCTAGAGAAATTCAAATTTGGATGCATCTGTAATAAACT 465
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 466 CACTCAGGCCTCAATTCATCTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT 525
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 526 ATTTTAAAGCTG---GGCAGACGATCAGCATCAAAAGAGCTGTTGGATAGACTGTGGT 582
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 583 ATTCATGCAAGAGATGGATTGGTCTCTGCTTTTGTGAGTGGTTTGTAAAGAGACTCTT 642
Qy 81 ----- 81
Db 643 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702
Qy 82 -----GlyHisAsnArgMetTrpArg 88
Db 703 ATGCCTGTGTTAAGCTGATGGATACCAATTTAGTTGGACCAATGATCGATTTTGAGA 762
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 763 AAACAGGTCAAGAACTCAAGTTTCGCTGCGGTGGAGTGGATGCCAATAGAAACTGG 822
Qy 109 AlaSerLysHisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrCys 128
Db 823 AAAGTGAAG---TGTGTGATGAAGAGCTCTATGACCCCTTGTGATGACACATACCTGT 879
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 880 GGCCCTTTTCAGAAATCGAGCCGGAAGTGAAGCTGTAGCTAATCTCTTCGAAACAC 939
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 940 AGAAAGCACATTAGGCTTATCTCTCTTTTCATGTCATATGTCATGATGTTTACTGTATCCC 999
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Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu 188
Db 1000 TATTTCTTACAAATPATGCAACAATTCCTCAATTTTAGATGTGTGGAATCTGCAGCTTATAA 1059
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1060 GCTGTGAATGCACTTTCAGTCAGTA---TACGGGGTACGATACAGATATGGACCAGCTCC 1116
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1117 ACAACGTTGTATGTAGCTCTGCTAGCTCAATGATGGCTTACAAATAATGGAATACCT 1176
Qy 229 TyrSerPhe----- 231
Db 1177 TATGCATTTGCTTTTCGAACCTACGTGACATGGATATTTGGATTTTACTCCAGAGATG 1236
Qy 232 -ThrSerAsnProProValGluLysLeu 240
Db 1237 CTCATCANACCCACCTGTACAGAACTA 1264

RESULT 13
US-10-274-639-33
; Sequence 33, Application US/10274639
; Publication No. US20030232349A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; GANDHI, Ameena R.
; APPLICANT: HAPALIA, April J.A.; LU, Dyang Aina M.
; APPLICANT: PATTERSON, Chandra; TRIBOLLY, Catherine M.
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.
; APPLICANT: NGUYEN, Darniel B.; LEE, Ernestine A.
; APPLICANT: KHAN, Farrah A.; YUE, Henry
; APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
; APPLICANT: POLICKY, Jennifer L.; RAMKUNAR, Jayalaxmi
; APPLICANT: YANG, Junming; THANGAVELU, Kavitha
; APPLICANT: DING, Li; KEARNEY, Liam
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.
; APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
; APPLICANT: BURFORD, Neil; WALIA, Narinder K.
; APPLICANT: LAL, Preeti G.; LEE, Sally
; APPLICANT: TODD, Stephen; LO, Terence F.
; APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.
; APPLICANT: AZIMZAI, Valda; LU, Yan
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0167 USA
; CURRENT APPLICATION NUMBER: US/10/274,639
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/22397
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/220,063
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,680
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,544
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,717
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/225,988
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/227,568
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1993
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030232349A1 4948403CB1
US-10-274-639-33
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## Alignment Scores:

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Pred. No.: 1.78e-62 Length: 1993
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 15 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-274-639-33 (1-1993)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg 25
Db 743 TATGAAGTTTATCACTCTCTTGAAGAAATTCAAATTTGGATGATCATCTGAATAAACT 802
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 803 CACTCAGCGCTCATTCACATGTTCTTATTGGAGATCATATGAGGAGGAGATCTCTTTT 862
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 863 ATTTTAAAGCTG---GGCAGACGATCAGCACTCAAGAGCTGTTTGGATAGACTGTGGT 919
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 920 ATTCATGCAAGAGATGATGATGTTGTCCTGCTTCTTGTGAGTGTGTTGTAAGAAAGCTCTT 979
Qy 81 ----- 81
Db 980 CTAACATATAAGATGACCCAGCCAGCATGAGAAATGTTGAATCATCTATATTTCTATATC 1039
Qy 82 -----GlyHisAsnArgMetTrpArg 88
Db 1040 ATGCTGTTTAACTGCGATGATACCAATTTTAGTTGGACCATGATGATTTTGAGA 1099
Qy 89 LysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAspPhe 108
Db 1100 AAAACAAGGTCAAGAACTCAAGGTTTCGCTGCGTGGAGTGGATGCAATAGAAACTGG 1159
Qy 109 AlaSerLysHisTrpCysGluGluGlyValSerSerSerSerSerGluThrTyrCys 128
Db 1160 AAGTGAAG---TGCTGTGATGAAGGAGCTTCTATGACCCCTGTGTGATGACACATCTGT 1216
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 1217 GGCCCTTTCCAGAACTGAGCGGAGTGAAGCTGTAGTAACCTCTCTCGAAACAC 1276
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 1277 AGAAAGCACATTAAGGCTTATCTCTCTTTCATGATGATGATGATGATGATGATGAT 1336
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 1337 TATTCCTTACAAATATGACAAATTTTACAAATTTTATGATGTTGGAAATCTGCAGCTTATAA 1396
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1397 GCTGTGAATGACCTTCAGTCAGTA---TACGGGTACATACATACATATGACAGCCCTCC 1453
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspTrpIleTyrAspLeuGlyIleLys 228
Db 1454 ACAACGTTGTATGAGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1513
Qy 229 TyrSerPhe----- 231
Db 1514 TATGCAATTTGCTTTCGAACCTACGTGACCTGGATATTTTGGATTTTACTCCAGAGATG 1573
Qy 232 -ThrSerAsnProProValGluLysLeu 240
Db 1574 CTCATCAAAACCCACTGTACAGAACTA 1601
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## RESULT 14

US-10-333-574-33

; Sequence 33, Application US/10333574

## Publication No. US20040091962A1

```
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DELEGANE, Angelo M.; GANDHI, Ameena R.
APPLICANT: HAPUZU, Chandra S.; TRIBOULEY, Catherine M.
APPLICANT: DAS, Debopriya; KALLICK, Deborah A.
APPLICANT: NGUYEN, Dannel B.; LEE, Ernestine A.
APPLICANT: KHAN, Farrah A.; YUE, Henry
APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi
APPLICANT: YANG, Junming; THANGAVELU, Kavitha
APPLICANT: DING, Li; KEARNEY, Liam
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
APPLICANT: BURFORD, Neil; CHAWLA, Narinder K.
APPLICANT: LAL, Preeti G.; LEE, Sally
APPLICANT: TODD, Stephen; LO, Terence P.
APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.
APPLICANT: AZIMZAI, Valda; LU, Yan
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0167 USN
CURRENT APPLICATION NUMBER: US/10/333,574
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 01/22397
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/220,063
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/221,680
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,544
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/224,717
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/225,988
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 60/227,568
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 1993
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 4948403CB1
US-10-333-574-33

Alignment Scores:
Pred. No.: 1.78e-62 Length: 1993
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 15 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-333-574-33 (1-1993)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg 25
Db 743 TATGAAGTTTATCACTCTCTTGAAGAAATTCAAATTTGGATGATCATCTGAATAAACT 802
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 803 CACTCAGCGCTCATTCACATGTTCTTATTGGAGATCATATGAGGAGGAGATCTCTTTT 862
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 863 ATTTTAAAGCTG---GGCAGACGATCAGCACTCAAGAGCTGTTTGGATAGACTGTGGT 919
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
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Db 920 ATTCAATGACAGAGAAATGGATTGGCTGCTGCTTTTGTGTCAGTGGTTGTAAAGAAGCTCTT 979
Qy 81 -----
Db 980 CTAACATATAAGAGTGCACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 1039
Qy 82 -----
Db 1040 ATGCTGTGTTAACTGTCGATGATACCATTTTAGTTGGACCAATGATCGATTTTGAGGA 1099
Qy 89 LysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 1100 AAAACAGGTCAGGAACCTCAAGTTTCGCTGCGTGAGTGGAATGCCAATAGAAATGG 1159
Qy 109 AlaSerLysHisThrCysGluGluGlyAlaSerSerSerSerSerGluThrTyrCys 128
Db 1160 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGACCCCTTGTGATGACACATACCTGT 1216
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
Db 1217 GGCCCTTTTCAGAAATCTGAGCCGGAAGTGAAGCTGTAGCTAACTTCTCTTCGAAAAACAC 1276
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 1277 AGAAGCACATAGGCTTAATCTCTCTTTCATGCATATGCTCAGATGTTACTGTATCCC 1336
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 1337 TATCTTACAATAATGCAACAATTCCTCAATTTAGATGTGTGGAATCTGCGAGCTTATATA 1396
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1397 GCTGTGAATGCATTCAGTCACTAGTA---TACGGGTGACGATACAGATATGGACCGCTCC 1453
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTyrPileTyrAspLeuGlyIleLys 228
Db 1454 ACAAGTTGTATGAGAGCTGTGTTAGTCAATGATGGGCTACAAATATGGAATACCT 1513
Qy 229 TyrSerPhe-----
Db 1514 TATGCAATTTGCTTGAACACTAGTGACACTGGATATTTTGGATTTTACTCCACAGATG 1573
Qy 232 -ThrSerAsnProProValGluLysLeu 240
Db 1574 CTCATCAAAACCCACTGTACAGAAACTA 1601
RESULT 15
US-10-757-262-127
; Sequence 127, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Eliaso, Venkateswarlu
; APPLICANT: Eliaso, Scott D
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21185, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNOINM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
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; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (217)...(1530)
US-10-757-262-127
Alignment Scores:
Pred. No.: 3,05e-62 Length: 1907
Score: 554.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.44% Indels: 58
DB: 18 Gaps: 5
US-09-980-881A-4 (1-246) x US-10-757-262-127 (1-1907)
Qy 6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPileGluPheIleThrGluArg 25
Db 622 TATGAAGTTTATCTACTCTTAGAAGAAATCAAATTTGGATGCATCATCTGAATAAACT 681
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 682 CACTCAGGCTCATTCATCATGTTCTCTATTTGAAGATCATATGAGGAAGATGCTTTTT 741
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPileAspCysGly 65
Db 742 ATTTTAAAGCTG---GGCAGACGATCACACTCAAAAGAGCTGTTTGGATAGACTGGT 798
Qy 66 IleHisAlaArgGluTyrPileSerProAlaPheCysLeuTyrPheIle----- 81
Db 799 ATTATGCAAGAGAAATGGATTGGTCTGCTCTTTTGTTCAGTGGTTTGTAAAGAAGCTCTT 858
Qy 81 -----
Db 859 CTAACATATAAGAGTGCACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 918
Qy 82 -----
Db 919 ATGCTGTGTTTAACGTCGATGGATACCACTTTTAGTTGGACCAATGATCGATTTTGAGA 978
Qy 89 LysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 979 AAAACAGGTCAGGAACCTCAAGTTTCGCTGCGTGAGTGGAATGCCAATAGAACTGG 1038
Qy 109 AlaSerLysHisThrCysGluGluGlyAlaSerSerSerSerSerGluThrTyrCys 128
Db 1039 AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGACCCCTTGTGATGACACATACCTGT 1095
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn 148
Db 1096 GGCCCTTTTCAGAAATCTGAGCCGGAAGTGAAGCTGTAGCTTCTCTTCGAAAAACAC 1155
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
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Db 1156 AGAAGCACATTAGGGCTTATCTCTCTTCATGATATGCTCAGATGTTACTGTATCCC 1215
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 1216 TAITCTTACAAATATGCAACAATCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1275
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1276 GCTGTGAATGCACCTTCAGTCAGTA--TACGGGGTACGATACAGATATGGACCGCCTCC 1332
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1333 ACAACGTTGTATGTAGAGCTCTGTAGCTCAATGGATTGGGCTACAAAAATGGAATACCT 1392
Qy 229 TyrSerPhe----- 231
Db 1393 TATGCATTTGCTTTCGAACTACGTGACACTGGGATATTTTGGATTTTACTCCCGAGATG 1452
Qy 232 -ThrSerAsnProProValGluLysLeu 240
Db 1453 CTCATCAAAACCCACCTGTACAGAACTA 1480

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Job time : 436.415 secs

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